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#### Shears, Beverly

From:

Hamud, Fozia

Sent:

Monday, August 18, 2003 12:36 PM

To:

Shears, Beverly

Subject:

RE: Seq. Search Request

Sorry about that. It is SEQ ID NO:2. Thanks.

----Original Message-----

From:

Shears, Beverly

Sent:

Monday, August 18, 2003 12:34 PM

To:

Hamud, Fozia

Subject:

Seq. Search Request

Fozia,

You recently submitted a seq. search request for SN 09/892949; however, you omitted the Seq. ID to be searched. Your request reads:

Pls. search SEQ ID NO: from amino acid residue 20-227; 544-732; 520-543 against commercial data bases, thanks.

Which Seq. ID do you wish to search?

BEVERLY SHEARS USPTO BIOTECH/CHEM LIBRARY CM-1, RM 1EO5 703-308-4994 BEVERLY.SHEARS@USPTO.GOV THIS PAGE BLANK (USPTO)

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Sequence:
                        Title:
Perfect score:
                                                                                                                                                                                         OM protein - protein search, using sw model
                        US-09-892-949-2_COPY_20_227
1121
                                                                                      August 18, 2003, 13:12:37; Search time 79.0499 Seconds (without alignments) 417.649 Million cell updates/sec
1 ALPAKPENISCVYYYRKNLT.....SKFWSDWSQEKMGMTEEEAP 208
                                                                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c):1993 - 2003 Compugen Ltd.
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Scoring table: 1107863 seqs, 158726573 residues Gapop 10.0 , Gapext 0.5 BLOSUM62

Total number of hits satisfying chosen parameters:

1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database A Geneseq 19Jun03:\*

| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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1121	1121	1121	1121	1121	1121	1121	1121	1121	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query
649	627	582	582	582	581	549	548	324	Query Match Length DB
23	24	23	23	23	24	24	24	23	BB
ABB05738	ABP54366	AAU83637	ABB85002	ABB95608	ABP54367	ABP54368	ABP54369	ABB05732	IJ
Human zcytor17 pro	. Human NR10.5 splic	Human PRO protein,	Human PRO21384 pro	Human angiogenesis	Human NR10.6 splic	Human NR10.7 splic	Human NR10.8 splic	Zcytor17 soluble f	Description

8. 5	268.5	8.5	8.5	8 5	æ 5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	1.5	1.5		2.5		.5	.5	2.5	110			21	_	μ.	_	_	_	_	1	1121	1121	21
24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.2	24.2	26.3	44.8	44.8	44.8	44.8	44.8	99.0	99.0	99.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
918	918	918	859	859	809	738	727	708	658	488	488	332	332	917	917	77	726	716	716	662	547	252	252	239	764	764	764	745	732	189	662	662	662	652	652
17	15	12	21	20	23	21	21	17	17	23	22	21	20	21	13	23	23	24	24	23	23	23	22	23	24	24	23	23	23	24	23	23	22	23	22
AAR75368	AAR46233	AAR10545	AAY92184	AAW70796	AAU75498	AAY92194	AAY92192	AAR85911	AAR94576	AAE23860	AAE12610	AAY92188	AAW70799	AAY55073	AAR26334	AAE24022	AAE24037	ABP54371	ABP54370	ABB05742	ABB05745	AAE24027	AAB51243	ABB05733	ABP54365	ABP54364	ABB05743	AAE24024	ABB05730	ABP54363	ABB05741	AAE24029	AAB51244	AAE24028	AAB51242
Human gp130 protei	$\mathbf{L}$	binant	gp130-					7	gp130 splic	Ob re	gp130	gp130	gp130-delta	gp130		Human HPR1 protein	Mouse haematopoiet		mNR10Balk	zcytor17	zcyt	_	haemopo	zcytor	NR10	NR10.4	zcytor	_	zcytori	NR1	zcytor17	-	Human haemopoietin	Human HPR1 variant	Human haemopoietin

## ALIGNMENTS

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	inflammatory disease; pancreatitis; inflammatory bowel disease.	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;	<pre>muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;</pre>	antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;	<pre>Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;</pre>		Zcytor17 soluble form truncated in the fibronectin domain SEQ ID NO:18.		01-MAY-2002 (first entry)		ABB05732;		ABB05732 standard; Protein; 324 AA.	ABB05732	RESULT 1

26-JUN-2000; 2000US-214282P 29-JUN-2000; 2000US-214955P 08-FEB-2001; 2001US-267963P Sprecher CA, Homo sapiens. 26-JUN-2001; 2001WO-US20484. 03-JAN-2002. WO200200721-A2 (ZYMO ) ZYMOGENETICS INC. Presnell SR, Gao Z, Whitmore TE, Kuijper JL;

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RESULT 2
ABP5436
XX ABP5
XX ABP5
XX ABP5
XX ABP5
XX ABP5
XX Huma
XX NR10
XW haem
KW haem
KW haem
XX Homo
XX Homo
XX WO20
PD 03-C
PD 03-C
XX
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                                                                                                                                                             NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic cell regulation.
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                    22-MAR-2002; 2002WO-JP02769
                                                       03-OCT-2002.
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)B; ABA93781.
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ilarity 100.0%;
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Pred. No. 2.7e-103;
; Mismatches 0;
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                       26-MAR-2001; 2001JP-0087298
                                                 22-MAR-2002; 2002WO-JP02769
                                                                                                     WO200277230-A1
                                                                                                                                                       haematopoietic
                                                                                                                                                                    NR10; splicing variant; haematopoietin receptor; immunomodulator; haematic; haematopoietic factor; immunological disease;
                                                                                                                                                                                                          Human NR10.7 splicing variant protein
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                                                                                                                                                                                                                                                               ABP54368;
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DB; ABQ83369.
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5.7e-103;
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(CHUS ) CHUGAI SEIYAKU KK

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RESULT 4
ABP54367
ID ABP54367
XX ABP54367
XX ABP5
XX ABP5
XX NR10
DE Huma
XX NR10
KW Inaen
KW Inaen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.7 protein from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human NR10.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP54367;
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                              Maeda M,
                                                                                                                                                                                                                                              03-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                         haematopoietic
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                                                                                                                                    26-MAR-2001; 2001JP-0087298
                                                                                                                                                                                         22-MAR-2002; 2002WO-JP02769.
                                                                              (CHUS ) CHUGAI SEIYAKU KK.
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                            Yaguchi N,
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                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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                            Hasegawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variant protein
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Pred. No. 5.7e-103;
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RESULT 5
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Best Local
20-JUL-2000;
25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.6 protein from the present invention.
                                                                                                                                                                                                                                                            Human; angiogenesis; PRO protein; cardiovascularisation; woun atherosclerosis; cardiac hypertrophy; gene therapy; endotheli cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-018925/01.
N:PSDB; ABQ83367.
                                                                                                                                                              31-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing
                                                                                                                                 09-JUL-2001;
                                                                                                                                                                                        WO200208284-A2
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                 antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                       Human angiogenesis related protein PRO21384 SEQ
                                                                                                                                                                                                                                                                                                                                                      19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                   ABB95608;
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2000US-219556P.

2000US-22064P.

2000US-220664P.

2000WO-US20710.

2000WS-222695P.

2000WS-222695P.

2000WS-222695P.

2000WS-US23522.

2000WS-US23328.
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                                                                                                                                 2001WO-US21735
                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Pred. No. 6.2e-103;
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Best Local Similarity
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25-MAY-2001;
25-MAY-2001;
25-MAY-2001;
30-MAY-2001;
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18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
24-OCT-2000;
08-NOV-2000;
01-DEC-2000;
01-DEC-2000;
20-DEC-2000;
20-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Fe
Godowski PJ,
Stephan JF,
                                                                                                  The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial rescenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
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(BACE)
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(MANTA/)
(PAON/)
(STEP/)
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10-MAY-2001;
                                                               Sequence
                                                                                                                                                                                                                                                                                                                                    One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2001;
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)B; ABL95746.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
WOOD W I.
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GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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BAKER K P.
FERRARA N.
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2000US-0664610
2000US-0665350.
2000US-0665350.
2000US-07923B.
2000WO-US30952.
2000WO-US32678.
2000WO-US32678.
2000WO-US32678.
2000US-0747259.
2001US-0767609.
2001US-0767609.
2001US-0767609.
2001US-0806666.
2001US-080666.
2001US-080666.
2001US-080666.
2001US-080666.
2001US-080666.
2001US-080666.
2001US-080666.
2001US-08066.
2001US-08066.
2001US-0806.
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  100.0%;
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L, Hillan KJ, Marsters SA,
CK, Williams PM, Wood WI,
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  Score
Pred.
  1121; DB 23;
No. 6.2e-103;
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A, Pan J,
Ye W;
                     Length
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23-JUN-2000

25-JUL-2000

25-JUL-2000

26-JUL-2000

27-JUL-2000

27-JUG-2000

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27-JUG-2000

27-JUG-2000

27-JUG-2000

27-SEP-2000

27-SEP-2000

27-SEP-2000

27-SEP-2000

27-SEP-2000

27-SEP-2000

27-SEP-2000

28-PED-2000

29-DEC-2000

20-DEC-2000

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21-MAR-2001

21-MAR-2001

21-MAR-2001

22-MAR-2001

23-MAR-2001

24-MAR-2001

25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; antiarteriosclerotic; PRO agonist; PRO antiagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                                                                                                                                                                                                                                                                                          20-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO21384 protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
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2000US-219556P.
2000US-220664P.
2000US-220664P.
2000WO-US20710.
2000US-222695P.
2000US-0643657.
 2000US-230978P.
2000US-06665150.
2000US-0665350.
2000US-242922P.
2000WO-US30952.
2000WO-US30952.
2000WO-US30973.
2000WO-US32678.
2000WO-US32678.
2000WO-US324956.
2001US-0767609.
2001WS-0767609.
2001WS-0766520.
2001WG-0806520.
2001WG-0806520.
2001US-080666.
2001US-080666.
2001US-080666.
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2000WO-US23328.
2000US-230978P.
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Best Local
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Godowski PJ,
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10-MAY-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertrension, arterial restenosis, rheumatoid arthritis, anglina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder mammanl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 ABB85003. The PRO proteins and polymucleotides have cardiant, cantiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2001;
30-MAY-2001;
                                                                                                                       AAU83637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                             08-MAY-2002
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)B; ABL88257.
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                             PRO protein, Seq ID No
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secreted protein; PRO; tumour; lung cancer; colon cancer;
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                                                                                                                     standard;
                                                                                                                                                                                                                                                                       IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI 180
                                                                                                                                                                                                                                                                                                                                SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
                                                                                                                                                                                                                                                                                                                                                                       ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA 111
                                                                                                                                                                                                                                                                                                                                                                                           ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
                                                                                                                                                                                                                             ALRCAVKESKFWSDWSQEKMGMTEEEAP
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                                                                                                                                                                                                                                                      IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 AA;
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2001US-0854280.

2001US-0866028.

2001US-0866034.

2001US-0870574.

2001US-0870574.
                                                          (first entry)
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L, Hillan KJ, Ma
CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1121; DB 23;
Pred. No. 6.2e-103;
); Mismatches 0;
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PM, Wood WI,
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Ye W;
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1 ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA

Matches Query Match Best Local

Similarity

100.0%;

Score 1121; DB 23; Pred. No. 6.2e-103; ; Mismatches 0;

Indels Length

0;

Gaps

60 0

Conservative

0;

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The invention relates to one hundred and twenty two nucleic acids
cencoding PRO polypeptides. The sequences of the 122 PRO polypucleotides
cencode human secreted proteins. The PRO nucleic acids, polypeptides,
cencode human secreted proteins. The PRO nucleic acids, polypeptides,
cencode human secreted proteins. The PRO nucleic acids, polypeptides,
cencer, colon cancer, breast tumour, prostate tumour, rectal tumour or
cencer, colon cancer, breast tumour, prostate tumour, rectal tumour or
cencer, colon cancer, breast tumour, prostate tumour, rectal tumour or
cencer, colon cancer, breast tumour, prostate tumour, rectal tumour or
cencer, colon cancer, breast tumour, prostate tumour, rectal tumour or
cencer, colon cancer, breast tumour, prostate tumour, rectal tumour or
central tumour or for security the proliferation of, or gene expression, in pericyte cells, for stimulating the
central central colon cancer, breast tumour necrosis factor-alpha from human blood,
for stimulating the release of tumour necrosis factor-alpha from human dermal
central centr
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25-JUL-2000
26-JUL-2000
28-JUL-2000
23-JUG-2000
23-JUG-2000
24-JUG-2000
15-SEP-2000
10-NOV-2000
28-NOV-2000
01-DEC-2000
01-DEC-2000
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28-FEB-
10-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -
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Grimaldi JC,
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-172001/22.
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25-JUL-2000;
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                                                                        in chromosome and gene mapping.
tein sequences of the invention.
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C, Gurney
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2000WG-US20710;

2000WG-US23522.

2000WG-US23522.

2000WG-US23328;

2000WG-US233873;

2000WG-US23646P.

2000WG-US2678;

2000WG-US2678;

2000WG-US2678.
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2000US-220605P.
2000US-220607P.
2000US-220624P.
2000US-220638P.
2000US-220664P.
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2001WO-US17092
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Smith V, Stephan JF, Watanabe
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tanabe CK,
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K. Wood WI;
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                                                      Matches
                                                                 Query Match
Best Local (
                                                                                                                                               The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.5
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200277230-A1
                                                                                                                                      protein from the present invention.
                                                                                                                                                                                                                                                                                                             remedies
                                                                                                                                                                                                                                                                                                                          genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoietic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHUS )
                                                                                                                                                                                                                                                                                                         splicing variants of hematopoietin receptor proteins and encoded s, applicable in searching hematopoietic factors and developing dies for immunological and hematopoietic diseases
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52
                                                      208;
                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                              Fig 10-12; 250pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRXDKNQTYNLTGLQPFTEYVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
              ALPAKPENISCVYYYRKNITCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
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                                                                                                                                                                                                                                                                                                                                                                                                         Yaguchi N,
                                                                                                            627 AA;
                                                   100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing variant protein
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                                                 Score 1121; DB 24;
Pred. No. 6.9e-103;
; Mismatches 0;
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RRSULT 9
ABB05738
AB 1D
ABB05738
AB 1D
AB 20
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AB 4D
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                CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antiarheumatic, antiarthritic and muscular activities. The zcytor17 CC proteins are useful for treating and diagnosing lymphoid, immune, CC inflammatory, spleenic, blood or bone disorders. Agonists or CC anti-zcytor17 antibodies are useful in stimulating cell-mediated CC immunity and for stimulating lymphocyte proliferation, such as in the CC treatment of infections involving immunosuppression, including certain CC viral infections. They are also useful for inducting cytotoxicity and CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiirinflammatory; antiiriral; antirheumatic; antiarthritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotide useful for treating and spleenic, blood or bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 195-197; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maurer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001;
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29-JUN-2000;
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2000US-214955P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zcytor17 which inflammatory,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                     The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and pollen allergy.
                                                                                                                                                                                             Hematopoietin receptor protein NR10 for screening potential ligands treatment of immune and hematopoietic disorders such as autoimmune
                                                                                                                                                                                                                                     WPI; 2001-061720/07.
N-PSDB; AAC92337.
                                                                                                                                                                                                                                                                                                                              02-JUN-1999;
30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human haemopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB51242;
                                                                                                                                                      Claim 1; Fig 3-5; 127pp; Japanese
                                                                                                                                                                                   diseases
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                                                                                                                                                                                                                                                                                                     (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmemb immune disorder; haematopoietic disorder; autoimmune diseas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergy; pollen allergy.
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                                                                                                                                                                                 immune and allergies -
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99JP-0217797.
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Pred. No. 7.2e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulation; transmembrane;
der; autoimmune disease; allergy;
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Sequence

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The present invention relates to human and murine haematopoietin receptory polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for

haematopoietin receptor

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                 pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; osteoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
                                                                                                  Human and murine hematopoietin receptor useful for treating cell proliferation, hormone related conditions -
                                                                                                                                                                                                                              06-OCT-2000; 2000US-238706P
13-OCT-2000; 2000US-240476P
20-FEB-2001; 2001US-270282P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation
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                                                                                                                                                                                                                                                                                                                                                                                        disease;
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                                                                                                                                                                            Mosley BA,
                                                                       Page 110-112; 136pp;
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CC treating cell proliferation conditions such as leukaemia and tumour CC metastasis, osteoporosis resulting from an excess of bone-resorbing CC cells. HPR sequences are also useful for treating medical conditions and CC diseases such as cell proliferation, metabolic and reproductive hormone CC related conditions. They are useful for treating various haematologic and CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, CC squamous cell carcinoma (e.g., adenocarcinoma (for example, breast cancer), carcinoma (e.g., adenocarcinoma (for example, breast cancer), CC squamous cell carcinoma), haemacologic disorders, anaemias (e.g., anaemia CC dysplastic syndromes (including refractory anaemia, refractory anaemia CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-paenic purpura (ITP), sickle cell vacess blasts), idiopathic thrombosis/
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such cancer in toth loss of the content of the process of the content of the co
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14-DEC-2000
                                                                                  WO200075314-A1
                                                                                                                                                                                                                                                                                                                                  Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.
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01-JUN-2000; 2000WO-JP03556.

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                                          Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation; pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; osteoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; TTP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitits; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haemotopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the
                                                                                                                                                                                                                                                                                                                                      AAE24029 standard; Protein; 662
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30-JUL-1999;
                                                                                                                                                                                                                                  Human HPR1 variant protein #3.
                                                                                                                                                                                                                                                                     23-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and pollen allergy.
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99JP-0217797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1121; DB 22; 100.0%; Pred. No. 7.5e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              CC oncologic disorders e.g., Epstein-Barr virus positive nasopharyngeal
CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
CC of Chronic disease, aplastic anaemia, Fanconi's aplastic anaemia,
CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
CC as osteoporosis including refractory anaemia, periodontitis
CC resulting in tooth losesning or loss, prosthesis losesning after joint
CC as osteoporosis including post-menopausal osteoporosis, periodontitis
CC resulting in tooth losesning or loss, prosthesis losesning after joint
CC dementia including Creutzfald-Jacob disease, demyelinating neuropathy,
CC demitia in-Barre syndrome, vertebral disc disease, Gulf war syndrome,
CC myasthenia gravis, chronic neuronal degeneration, stroke including
CC cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
CC deficient mammary development and infertility. The present sequence
CC is human HPR1 variant protein
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematologic and oncologic disorders a general sequence of the order and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human and murine hematopoietin receptor polypeptides HPR1 and HPR2, useful for treating cell proliferation, metabolic, and reproductive hormone related conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2000; 2000US-238706P.
13-OCT-2000; 2000US-240476P.
20-FEB-2001; 2001US-270282P.
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human and murine haematopoietin recepton polypeptides HPR1 and HPR2. Sequences of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 112-115; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosman DJ, Mosley BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                         208;
      153
                                              121
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G
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
                                                                                                                                                                                              ALPAKPENISCVYYYRKNIICTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
                      IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
                                                                                                                                                                   ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
                                                                                 SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 152
IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
                                                                                                                                                                                                                                                                                                                                             662 AA;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                   protein.
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                                                                                                                                                                                                                                                     Score 1121; DB 23;
Pred. No. 7.5e-103;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                             Length 662;
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1 ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA

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Gaps

60 0

Conservative

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RESULT 14
ABB05741
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                                                                            cc antirheumatic, antiarthritic and muscular activities. The zcytor17
cc proteins are useful for treating and diagnosing lymphoid, immune,
cc inflammatory, spleenic, blood or bone disorders. Agonists or
anti-zcytor17 antibodies are useful in stimulating cell-mediated
cc inmunity and for stimulating lymphocyte proliferation, such as in the
creatment of infections involving immunosuppression, including certain
cviral infections. They are also useful for inducting cytotoxicity and
cf or treating leukopenias. Antagonist of zcytor17 polypeptides are useful
cf or treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
colleges), inflammatory diseases (e.g. Crohn's disease), cancer,
cp pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
ABA93843 and ABB05730 to ABB05745 represent sequences used in the
cexemplification of the present invention.
 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotide encoding a cytokine receptor zcytor17 which useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2000; 2000US-214282P.
29-JUN-2000; 2000US-214955P.
08-FEB-2001; 2001US-267963P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
                                                   Sequence
                                                                                                                                                                                                                                                                                                                         The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 204-206; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-090519/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001; 2001WO-US20484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inrection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human zcytor17 protein sequence SEQ ID NO:54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB05741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB05741 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory
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Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
 Similarity
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                                                   662 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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100.0%;
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Score 1121; DB 23; Pred. No. 7.5e-103;
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               Length
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ID ABP54
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AC ABP54
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NR10
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                                                                                                                       Query Match
Best Local S
Matches 208
                                                                                                                                                                                                                                                                                                 The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.3 protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic cell regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 3; 250pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-018925/01.
N-PSDB; ABQ83363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NR10.3 splicing variant protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001; 2001JP-0087298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2002; 2002WO-JP02769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
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   52
                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA 111
                                   ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALRCAVKESKFWSDWSQEKMGMTEEEAP 240
                                                                                                                                                                                                                                              681 AA;
                                                                                                                100.0%; Score 1121; DB 24; ilarity 100.0%; Pred. No. 7.8e-103; Conservative 0; Mismatches 0;
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                                                                                                                                                                                 Length 681;
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                                                                                   IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI 180
                                                                                                                                                  SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
                                                                                                                                 SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM
                                                              IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
ALRCAVKESKFWSDWSQEKMGMTEEEAP
259
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Search completed: August 18, 2003, 13:27:00 Job time: 80.0499 secs

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Result
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Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 200000000
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Perfect score:
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        Score
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-08-123D-5
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US-08-838-524B-5
US-09-312-611-4
US-09-058-264-2
US-09-058-264-2
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Sequence 10, Appl
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Sequence 4, Appli
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Sequence 2, Appli
Sequence 7, Appli
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Sequence 6, Appli
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Sequence 9, Appli
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				Query Ma Best Loc Matches	CURRENT A CURRENT F PRIOR APP PRIOR FIL PRIOR FIL UNMBER OF SOPTWARE: SOPTWARE: SEQ ID NO LENGTH: TYPE: PR ORGANISM	RESULT 1 US-09-313-5 US-09-313-5 ; Sequence ; Patent NC ; GENERAL 1 ; APPLICAL ; APPLICAL ; TITLE OB ; TITLE OB ; FILE RBB		44444 8000 1000 1000 1000 1000 1000 1000
172 LQP  :  289 LKP	112 KI 231 II	53 SS	3 PJ   126 PI	/ Match Local Simi nes 66;	URRENT APPLICATIO URRENT FILING DATE: RIOR APPLICATION RIOR FILING DATE: RIOR FILING DATE: RIOR FILING DATE: UMBER OF SEQ ID N OFTWARE: FastSEQ Q ID NO 10 LENGTH: 332 TYPE: PRT ORGANISM: Homo sa 9-313-942-10	10, 10, 10, 10, 10, 10,		231 231 231 231 231 231 230 230 230 230 230 230 230 230 230 230
OPTEYVI         -	KPVLGIKRMIQIBWIKPBLAPVSSD : ::::     :   INSEELSSILKLTWINPSIKSVII-	SSTSENRAS	KPENISC	nilarity Conserva	T APPLICATION NUMBE T FILING DATE: 199 APPLICATION NUMBER: FILING DATE: 1999-0 APPLICATION NUMBER: FILING DATE: 1998-0 OF SEQ ID NOS: 32 RE: FastSEQ for Win NO 10 H: 332 PRT ISM: Homo sapiens	42-10 10, Applicat 10, Applicat 10, 6472179 NFORMATION: TI REGENERON INVENTION: INVENTION: INVENTION: ERENCE: REG		00000000000000000000000000000000000000
ALRCAVK	IQIEWIK	CSFFLPR : : VYFV	CVYYYRKO :   CIVNEGKX	24. 30. vative	NUMBER: 1999- MBER: 0 999-05- MBER: 0 998-09- : 32 r Windc	N N P.		3 8 8 9 3 8 8 9 8 9 8 9 8 9 8 9 9 9 9 9
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LQPFTEYVIALRCAVKESK-FWSDWSQEKMGMTEBEAP  :	LAPVSSDLKYTLRERTVNSTSWMEVNF:         :::  ::   ::   ::   ::   ::	IPDNYTIEVBAENGDGVIKS-HMTYWRLENIA                 : : : :  NIEVWVBAENALGKVTSDHINFDPVYKV-	PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK- 	Score 268.5; DB Pred. No. 3.3e-21 47; Mismatches 7	US/09/313,942 5-19 /313,942 9 /101,858 5 5 7 Version 3.0	ON US/09313942  PHARMACEUTICALS, INC. BECEPTOR BASED ANTAGONISTS, AND USING 03-A	ALIGNMENTS	US-09-071-224-20 US-09-071-224-17 US-09-071-224-25 US-09-071-224-2 US-09-071-224-2 US-09-071-224-2 US-09-071-224-2 US-09-071-224-23 US-09-071-224-27 US-09-071-224-21 US-09-071-224-21 US-09-071-224-30 US-09-071-224-6
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208 326 .	KPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTG 1:::: :::::::::::::::::::::::::::::::	KTEPPKIFRV        KPNPPHNLSV	PAKPENISCVYYYRKNLICTWSPGKETSY-TQYTVKRTYAFGEKHDNCTTN 5	Length 332; Indels 29; Gaps		METHODS OF MAKING		Sequence 20, Appl Sequence 17, Appl Sequence 22, Appl Sequence 25, Appl Sequence 2, Appli Sequence 4, Appli Sequence 21, Appli Sequence 21, Appli Sequence 27, Appli Sequence 28, Appli Sequence 28, Appli Sequence 31, Appli Sequence 31, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli
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RESULT 2
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.

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RESULT 3
US-09-069-781B-5
; Sequence 5, Application U:
; Patent No. 6287782
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REGISTRATION NUMBER: 37,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
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MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson,
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TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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APPLICATION NUMBER:
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TELEX: 200154
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                                                                                                                                                                                                                                                                                                                                         53 SSTSENRASCSFFLPRITIPDNYTIEVBAENGDGVIKS-HMTYWRLENIAKTEPPKIFRV 111
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                                                                                                                                                LKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRP 297
                                                                                                                                                                                                                                                                                                          YST-----VYFV-----NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV 201
                                                                                                                                                                                                                                                                                                                                                                                      PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD 156
                                                                                                                                                                                                                                                                                                                                                                                                                           PAKPENISCVYYYRKULTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTIN 52
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                                                 US/09069781B
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; Pred. No. 5.7e-21;
47; Mismatches 76;
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Best Local S
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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APPLICANT: Ctipeper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: proi
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 11-DEC APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meiklejohn, Ph.D., Anita L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 28-DE
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                                                                                                                                                                                                                                          ocal Similarity
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                                                                         157 YŚT-----VYFV-----NIEVWVEAENALGKVTŚDHINFDPVYKV-KPNPPHNLSV
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                                  KPVLGIKKMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTG 171
                                                                                                          SSTSENRASCSFFLPRITIPDNYTIEVEAENGDGVIKS-HMTYWRLENIAKTEPPKIFRV 111
                                                                                                                                               PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD 156
                                                                                                                                                                  PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
INSEELSSILKLTWTNPSIKSVII-LKYNIQYRTKDASTWSQIP-PEDTASTRSSFTVQD 259
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 08/570,142
11-DEC-1995
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28-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1
                                                                                                                                                                                                                                          24.0%; Score 268.5; DB 3 30.3%; Pred. No. 5.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/569,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/599,455
1-1996
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                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                           Length 488;
                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                         Gaps
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US-09-137-132-5
                                                         ; MOLECULE TYPE: protein US-09-137-132-5
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FILING DATE: 18-AUG-1998
PROR APPLICATION UNMBER: 08/864,564
APPLICATION UNMBER: 08/864,564
APPLICATION UNMBER: 08/864,564
APPLICATION UNMBER: 28-May 08/864,564
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            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                               TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                               REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                            NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                           FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                        TOPOLOGY:
                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/569,485 FILING DATE: 08-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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5. 6380363
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                                                                                                      amino acid
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                                                                                                                   488 amino acids
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                                                                                                                                                                                  617-542-8906
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Tepper, Robert I.
   Conservative
                                                                                          unknown
                                                                                                                                                                                                                                                                                                                           04-DEC-1995
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              24.0%;
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   47;
                                                                                                                                                                                                                                 07334/019004
Score 268.5; DB 4;
Pred. No. 5.7e-21;
7; Mismatches 76;
                            Length 488;
 Indels
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29;
Gaps
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US-08-864-564A-5
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Patent No.
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                                      INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 03-SEP-1996
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                    SEQUENCE CHARACTERISTICS
                                                                                                                                                   FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Ani
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                               APPLICATION NUMBER: 08/583
FILLING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570
FILLING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/566
FILLING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566
FILLING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/566
FILLING DATE: 27-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                              REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/6: FILING DATE: 26-APR-1996 APPLICATION NUMBER: 08/5: FILING DATE: 22-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 02110-2804
                                                           TELEX:
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488 amino acids
                                                                             617-542-8906
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Culpepper, Janice A.
White, David W.
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                                                                                                                                     07334/019002
                                                                                                                                                                          Anita L.
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APPLICANT: Tartagl:
APPLICANT: Tepper,
APPLICANT: Culpepp
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Culpepper, Jan
APPLICANT: White, David W
TITLE OF INVENTION: THE O
TITLE OF INVENTION: THE D
TITLE OF INVENTION: INCLU
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                            FILING DATE: 09-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                           APPLICATION NUMBER: PILING DATE: 28-MAN APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEB: Fish a ......
STREET: 225 Pranklin Street
                              APPLICATION NUMBER: 08/5
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/5
                                                                                                                            FILING DATE: 22-JAN APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE:
APPLICATION 1
                                                                              APPLICATION NUMBER: 08/5
                                                                                                                FILING DATE:
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                                                                                                                                                              PPLICATION NUMBER:
                                                                                                                                                                                           PPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                             02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YST-----VYFV-----NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD
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                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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 NUMBER:
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28-МАУ-1997
               04-DEC-1995
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                              08/566,622
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08/562,663
                                                             08/569,485
                                                                                               08/570,142
                                                                                                                                                                                              08/638,524
                                                                                                                                                                                                                                                                                                           US/09/094,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Janice A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 268.5;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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.5.7e-21;
.76;
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Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08708123D
Patent No. 6482927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tartag
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                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 26-APR-19
APPLICATION NUMBER: 08
FILING DATE: 22-JAN-19
APPLICATION NUMBER: 08
                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
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APPLICANT:
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                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fign w .... crneet
                                                                                                                                FILING DATE: 03-SEP-1996
                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07
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REGISTRATION NUMBER:
                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                   COMPUTER:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 LOPFTEYVIALRCAVKESK-FWSDWSQEXMGMTEEEAP 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 YST-----VYFV-----NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Culpepper, Janice A. White, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tepper, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tartaglia,
                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                   Fish & Richardson, P.C.
                                                                                                                                                                                                                                 Diskette
                 28-DEC-1995
                                                22-JAN-1996
                                                                            26-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                    THE OB RECEPTOR AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF INCLUDING OBESITY AND CACHEXIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.0%;
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                             08/583,153
                                                              08/599,455
                                                                                               08/638,524
                                                                                                                                                 US/08/708,123D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Louis A.
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FILING DATE:

11-DEC-1995

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Best Local Similarity
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APPLICANT: Tartag
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                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                         APPLICANT: Culpeppe
TITLE OF INVENTION:
TITLE OF INVENTION:
                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153A
FILING DATE: 28-DEC-1995
                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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LENGTH: 488 amino acid
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TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                 STREET: L. STREET: AL BOSTON
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APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
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                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD 156
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                                                                                                                                                                                                                                 225 Franklin Street
                                                                                                                                                                                  SD
                                                                                                                                                                                                                                                                                                                                                 Culpepper, Janice A.
                                                                                                                                                                                                                                                                                                                                                                  Tepper, Robert
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                                                                                                                                                                                                                                                                                                                                                                                  Tartaglia,
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                                                                                                                                                                                                                                                                                                                  THE OB RECEPTOR AND METHODS DIAGNOSIS AND TREATMENT OF
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                                                                                                                                                                                                                                                                                                                                                                                  Louis A.
08/570,142
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Pred. No. 5.7e-21;
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US-08-638-524B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                              CORRESPONDENCE
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                          STREET: 2-
STREET: Boston
                                                                                                                                                                                                                                                                                 TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meiklejohn, Anita L. REGISTRATION NUMBER: 35,283
                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Window
                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: unknown
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                                 APPLICATION NUMBER:
                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 YST------VYFV-----NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV
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5. 6548269
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                                                                                                                                                         02110-2804
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                                                                                                                                                                         S
                                                                                                                                                                                                                             225 Franklin Street
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Tepper, Robert I.
Culpepper, Janice A.
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                                                                                                                                                                                                                                                Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                  ADDRESS:
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                  26-APR-1996
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                                                                                                                                                                                                                                                                                                                  THE OB RECEPTOR AND METHODS FOR THE DISORDERS, INCLUDING OLD DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OLD
                                                                                   Windows95
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Sequence 4, Application US/0882558
Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lackin
NUMBER OF SEQUENCES: 14
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US-08-825-558-4
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                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, (
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283 REFERENCE/DOCKET NUMBER: 07334/018001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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APPLICATION NUMBER: 08/5
FILING DATE: 27-NOV-1995
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APPLICATION NUMBER:
FILING DATE: 11-DE
 APPLICATION NUMBER:
                                                                                                                                COUNTRY:
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                                                                                                                                                                                                      KESSLER, GOLDSTEIN & FOX
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US/08/825,558
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Pred. No. 5.7e-21
17; Mismatches 7
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RESULT 11
US-09-312-611-4
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Best Local Similarity
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APPLICANT: SHARKE
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                              FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: GP130 Lacking the Transmembrane
NUMBER OF SEQUENCES: 14
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LENGTH: 658 amino acid
                                                                      REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                     TELEFAX:
                                                      TELEPHONE:
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ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 YŚT-----VYFV-----NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                       WASHINGTON
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1100 NEW YORK AVENUE
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                                   (202) 371-2540
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                                                        (202) 371-2600
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30.3%; Pred. No. 8.8e-21;
                                                                                                                                                                                                                   US/09/312,611
                                                                                                              32,893
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                                                                                                 0623.0530002
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                                                                                                                                                                                                                                                           Version #1.30
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US-07-797-556-2
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                                                                                                           ; MOLECULE TYPE: protein US-07-797-556-2
                                               Matches
                                                               Query Match
Best Local (
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Patent No. 5262522
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Best Local S
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                                                                                                                                                                             TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                     ATTORNEY/ACENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gearing, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 658 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                   LENGTH:
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3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTTN
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                                                               Similarity
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AMINO ACID
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Receptor for Oncostatin M and Leukemia Inhibitory Factor

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; Pred. No. 8.8e-21;
47; Mismatches 76
                                               47; Mismatches
                                          Score 268.5; DB 1;
Pred. No. 9.8e-21;
                                                                                                                                                                                                                                                             2607
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US-08-308-881-2
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 12-SEP-19:
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,
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APPLICATION NUMBER: 1
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APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
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112 KPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTG 171
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                                                             186 YŚT-----VYFV-----NIEVWVEAENALGKVTŚDHINFDPVYKV-KPNPPHNLSV 230
                                                                                                                                        126 PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD 185
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                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                           PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
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                                                                                                                                                                                                               24.0%; Score 268.5; DB 1 ilarity 30.3%; Pred. No. 9.8e-21; Conservative 47; Mismatches 76
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese Katham
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 708 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cosman, I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/308,881 FILING DATE: 12-SEP-1994 APPLICATION NUMBER: US 08/249,553
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino
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 289
                                                                       231 INSEELSSILKLTWTNPSIKSVII-LKYNIQYRTKDASTWSQIP-PEDTASTRSSFTVQD
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                                                                                                                                           186 YST-----VYFV------NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV
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                                                                                                                                                                             53 SSTSENRASCSFFLPRITIPDNYTIEVEAENGDGVIKS-HMTYWRLENIAKTEPPKIFRV 111
                                                                                                                                                                                                                                                                                           66;
                                                                                                                                                                                                                                                     3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
                                LOPFTEYVIALRCAVKESK-FWSDWSQEKMGMTEEEAP 208
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LKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                       708 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mosley, Bruce
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunex Corporation
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                                                                                                                                                                                                                                                                                                            24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor for Oncostatin M
                                                                                                                                                                                                                                                                                         47; Mismatches
                                                                                                                                                                                                                                                                                                          Score 268.5; DB : Pred. No. 9.8e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2614-A
                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                           Length 708;
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US-09-059-099-2
                                                                                                                                                                                                                                                                                                                                                                           US-09-059-099-2
                                                                                                                                                                                                                                                                                                                 Query Match 24.0%;
Best Local Similarity 30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09059099 Patent No. 5925740
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 708 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple 7.1 SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 0
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mosley,
APPLICANT: Cosman,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
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                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
289
                                                                                                                                                186 YST-----VYFV-----NIEVWVEÄENALGKVTSDHINFDPVYKV-KPNPPHNLSV
                                                                      231 INSEELSSILKLTWTNPSIKSVII-LKYNIQYRTKDASTWSQIP-PEDTASTRSSFTVQD 288
                                                                                                                                                                                                                         126 PEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVD
                                                                                                                                                                                                                                                                                              66;
                                                                                                                                                                                    53 SSTSENRASCSFFLPRITIPDNYTIEVEAENGDGVIKS-HMTYWRLENIAKTEPPKIFRV 111
                                                                                                                                                                                                                                                            3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
                             LOPFTEYVIALRCAVKESK-FWSDWSQEKMGMTEEEAP
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                                                                                                           KPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTG
LKPFTEYVFRIRCMKEDGKGYWSDWSEBASGITYEDRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (206) 233-0644
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                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunex Corporation
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David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor for Oncostatin
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Pred. No. 9.8e-21;
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                    DB 2;
                                   208
                                                                                                                                                                                                                                                                                                                                 Length 708;
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Search completed: August 18, 2003, 13:32:20 Job time: 26.6912 secs

185

11

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Database :
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      August 18, 2003, 13:27:13; Search time 27.1734 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492763 segs, 131003257 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/pubpaa/PCT_\
/cgn2_6/ptodata/1/pubpaa/PCT_\
                                                                                          m2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US09_RUB_PUB.pep:*
m2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US0O_NEW_PUB.pep:*
m2_6/ptodata/1/pubpaa/US6O_NEW_PUB.pep:*
m2_6/ptodata/1/pubpaa/US6O_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                               _6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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1002.770 Million cell updates/sec
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and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	B	ID	Description
1	1121	100.0	324	11	US-09-892-949-18	Sequence 18,
N	1121	100.0	582	12	US-10-216-163-92	••
ω	1121	100.0	582	15	US-10-227-884-92	
4	1121	100.0	582	15	US-10-230-163-92	
ហ	1121	100.0	582	15	US-10-230-338-92	
0	1121	100.0	582	15	US-10-218-631-92	Sequence 92
7	1121	100.0	582	15	US-10-230-414-92	
œ	1121	100.0	582	15	US-10-216-159A-92	
9	1121	100.0	582	15	US-10-218-849-92	
10	1121	100.0	582	15	US-10-227-873-92	
11	1121	100.0	582	<u>1</u> 5	US-10-227-883-92	
12	1121	100.0	582	15	US-10-219-076-92	
13	1121	100.0	582	15	US-10-230-434-92	
14	1121	100.0	582	15	US-10-219-003-92	Sequence 92,
15	1121	100.0	лю	<u>,</u>	10 10 010 01	compand or

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
-10-216-160-	-085	-10 - 21	-234-	-10-232-229-	US-10-232-227-92	2-225-		0-230-436-	-10-22		US-10-227-880-92	-528-	US-10-219-524-92		-470-	9-072-	-205-	9-536-	-478-	-468-	-956-	165-		-231-	30-260-	-481-	US-10-219-479-92	-219-466-	US-10-219-464-92
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92,	372,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,	92,
App1	App	Appl	Appl	Appl	App1	Appl	App1	Appl	Appl	App1	App1	App1	App1	App1	Appl	App1	App1	Appl	App1	App1	Appl	App1	Appl	Appl	Appl	Appl	Appl	App1	Appl

## ALIGNMENTS

RESULT 1

Application US/09892949 US20030096339A1

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SEQ ID NO 18
LENGTH: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                Query Match 100.0%; Score 1121; DB 11; Length 324; Best Local Similarity 100.0%; Pred. No. 2.1e-104; Matches 208; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/214,955 PRIOR FILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sprecher, Cindy A. APPLICANT: Presnell, Scott R.
                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                  20
61 SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
                                                                                1 ALPAKPENISCVYYYRKNITCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA 60
                                                                                                                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version 3.0
                                                ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-92
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CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/05287
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063849
PRIOR APPLICATION NUMBER: 60/063849
PRIOR APPLICATION NUMBER: 60/063849
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 92
LENGTH: 582
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Publication No. US20030149239A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-03-27
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FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/064103
FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/079728
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FILING DATE: 1998-03-25
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                                          SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM
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SCSFFLPRITIPONYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM
                                                                                                                                                ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
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Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                        Score 1121; DB 12;
Pred. No. 4.6e-104;
; Mismatches 0;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C79
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/062549
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/084441
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FILING DATE: 1998-04-15
                                          APPLICATION NUMBER: 60/089905
FILING DATE: 1998-06-18
                                                                                                  APPLICATION NUMBER: 60/089538
                                                                                                                                                   FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/079728
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                                                                                    FILING DATE: 1998-06-
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                                                                                                                                                                                             APPLICATION NUMBER: 60/086392
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Smith, Victoria
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Grimaldi, J. Christopher
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Gerritsen, Mary
Goddard, Audrey
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FILING DATE: APPLICATION

1998-08-04 1998-07-07 1998-06-25 1998-06-25

1998-08-04

APPLICATION FILING DATE: FILING FILING FILING

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NUMBER:

1998-08-17

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1998-08-10

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APPLICATION NUMBER: 60/100385
                                                                                                                                              NUMBER: 60/108787: 1998-11-17
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NUMBER: 60/101738
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: 1998-08-31
                                                                      NUMBER: 60/108849
                                                                                                                                                                                                                         NUMBER: 60/106905
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NUMBER: 60/090691
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                                                                                          Query Match 100.0%; 9
Best Local Similarity 100.0%; 9
Matches 208; Conservative 0;
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OR APPLICATION NUMBER: 60/140723
OR APPLICATION NUMBER: 60/141037
OR APPLICATION NUMBER: 60/141037
OR APPLICATION NUMBER: 60/14758
OR FILING DATE: 1999-07-20
OR APPLICATION NUMBER: 60/145698
OR FILING DATE: 1999-07-26
OR APPLICATION NUMBER: 60/14622
OR APPLICATION NUMBER: 60/146963
OR APPLICATION NUMBER: 60/149320
OR APPLICATION NUMBER: 60/149320
OR FILING DATE: 1999-08-17
OR APPLICATION NUMBER: 60/149330
OR FILING DATE: 1999-08-17
OR APPLICATION NUMBER: 60/149330
OR FILING DATE: 1999-08-17
OR APPLICATION NUMBER: 60/151733
OR FILING DATE: 1999-08-31
OR APPLICATION NUMBER: 60/16418
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DR FILLING DATE: 1999-04-05
DR FILLING DATE: 1999-04-21
DR FILLING DATE: 1999-04-21
DR APPLICATION NUMBER: 60/131022
DR FILLING DATE: 1999-04-26
DR APPLICATION NUMBER: 60/131270
DR APPLICATION NUMBER: 60/131270
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DR FILING DATE: 1999-03-19
DR APPLICATION NUMBER: 60/125775
DR FILING DATE: 1999-03-23
DR APPLICATION NUMBER: 60/126773
DR FILING DATE: 1999-03-29
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 60/140650
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APPLICATION NUMBER: 60/115733
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APPLICATION NUMBER: 60/119549
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APPLICATION UNMER: 60/115558
FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115565
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FILING DATE: 1998-12-22
APPLICATION NUMBER: 60/113605
FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/113621
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  52
                         ALPAKPENISCVYYYRKNITCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA
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1999-01-12
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Pred. No. 4.6e-104;
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                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
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CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530P1C96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/063549
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/064103
OR APPLICATION NUMBER: 60/069873
OR APPLICATION NUMBER: 60/069873
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FILING DATE: 1998-04-15
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FILING DATE: 1997-09-17
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No. US20030036635A1
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Wood, William
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Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                            OR APPLICATION NUMBER: 60/101477
OR FILING DATE: 1998-09-23
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APPLICATION NUMBER: 60/099816
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APPLICATION NUMBER: 60/100390
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FILING DATE: 1998-09-10
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FILING DATE: 1998-08-17
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FILING DATE: 1998-09-17
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APPLICATION NUMBER: 60/099598
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FILING DATE: 1998-08-26
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                                                          NUMBER: 60/106905
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APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/095302 APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090691 NUMBER: 60/089905 1998-08-04 60/090472

FILING

1998-11-17

Matches

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Conservative

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Mismatches

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Indels

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PRIOR
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APPLICATION NUMBER: 60/169445
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APPLICATION NUMBER: 60/141037
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APPLICATION NUMBER: 60/115565
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APPLICATION NUMBER: 60/166361
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APPLICATION NUMBER: 60/146963
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APPLICATION NUMBER: 60/145698
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APPLICATION NUMBER: 60/131291
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APPLICATION NUMBER: 60/131022
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FILING DATE: 1999-03-10
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NUMBER:
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US-10-230-338-92
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                                                                             US-10-230-338-92
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APPLICANT: Baker, Ke
APPLICANT: Desnoyer
APPLICANT: Gerritse
                                                                                           SEQ ID NO 92
LENGTH: 582
TYPE: PRT
ORGANISM: Homo Sapien
                   Query Match
Best Local Similarity
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Matches 208;
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APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530P1C92

CURRENT APPLICATION NUMBER: US/10/230,338

CURRENT FILING DATE: 2002-08-28

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR PPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059119

PRIOR APPLICATION NUMBER: 60/053549

PRIOR APPLICATION NUMBER: 60/063549
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PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
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APPLICANT:
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C.
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APPLICATION NUMBER: 60/079656
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Wood, William I.
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Gerritsen, Mary
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   Conservative
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Score 1121; DB 15;
Pred. No. 4.6e-104;
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Query Match Best Local

Local Similarity

100.0%;

Score Pred.

1121; DB 15; No. 4.6e-104;

Length 582

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; LENGTH: 582
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; ORGANISM: Homo &
US-10-218-631-92
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PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR PPLICATION NUMBER: 60/063549
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
                                                                                      Query Match
Best Local Similarity
Matches 208; Conser
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 92
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CURRENT APPLICATION NUMBER: US/10/218,631
CURRENT FILING DATE: 2002-08-12
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FILING DATE: 1998-03-26
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FILING DATE: 1998-03-25
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                                      ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA 60
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                   ALPAKPENISCVYYYRKNLTCIWSPGKETSYTQYTVKRTYAFGEKHDNCTINSSTSENRA
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Godowski, Paul J
Grimaldi, J. Christopher
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Smith, Victoria
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                                                                                      Score 1121; DB 15;
Pred. No. 4.6e-104;
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-230-414-92
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US-10-230-414-92
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CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Desnoy
APPLICANT: Gerrit
APPLICANT: Goddar
APPLICANT: Godows
APPLICANT: Godows
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Best Local Similarity
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APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C98
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PRIOR APPLICATION NUMBER: 60/079728
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FILING DATE: 1997-12-17
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APPLICATION NUMBER: 60/064103
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61 SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-216-159A-92
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SEQ ID NO 92
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                          Local Similarity
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FILING DATE: 1998-03-25
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FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/079728
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121 IQIEWIKPELAPVSSDLKYTLRERTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
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Grimaldi, J. Christopher
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Gerritsen, Mary
Goddard, Audrey
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Smith, Victoria
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Pred. No. 4.6e-104;
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LENGTH: 582
TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 208; Conserv
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CURRENT FILING DATE: 2002-08-12
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                                                                                                                       Desnoyers, Luc
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                              Application US/10227873
No. US20030073816A1
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Godowski, Paul J.
Grimaldi, J. Christopher
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No. US20030073814A1
                                                                   Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L.
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Smith, Victoria
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Gerritsen, Mary
Stephan, Jean-Philippe Watanabe, Colin L. Wood, William I.
                                                   Smith, Victoria
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TITLE OF INVENTION: SECRETED AND TRANSMEMS TITLE OF INVENTION: ACIDS ENCODING THE SIFILE REFERENCE: P3530PL772
CURRENT APPLICATION NUMBER: US/10/227,873
CURRENT FILING DATE: 2002-08-26
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Publication No. US20030073817A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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DR APPLICATION NUMBER: 60/146222

DR FILING DATE: 1999-07-28

DR APPLICATION NUMBER: 60/146363

OR APPLICATION NUMBER: 60/146963

OR APPLICATION NUMBER: 60/149320

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Godowski, Paul J.
Grimaldi, J. Christopher
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Pred. No. 4.6e-104;
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CURRENT APPLICATION NUMBER: US/10/227,883
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
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PRIOR PILING DATE: 1997-12-17
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PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/079910
PRIOR APPLICATION NUMBER: 60/079994
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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PRIOR APPLICATION NUMBER: 60/079728
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR PILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-25
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PRIOR APPLICATION NUMBER: 60/084441
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APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C78
                                                                                                                                             R FILING DATE: 1998-08-04

R APPLICATION NUMBER: 60/095318

DR FILING DATE: 1998-08-04

R FILING DATE: 1998-08-08-10

DR APPLICATION NUMBER: 60/095916

DR APPLICATION NUMBER: 60/096146

DR APPLICATION NUMBER: 1998-08-11
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APPLICATION NUMBER: 60/085323
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/095302
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090691
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089905
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APPLICATION NUMBER: 60/086392
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/100848
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OR FILING DATE: 1999-06-22
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OR FILING DATE: 1999-06-22
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OR FILING DATE: 1999-06-23
OR APPLICATION NUMBER: 60/145698
OR FILING DATE: 1999-07-26
OR APPLICATION NUMBER: 60/145698
OR APPLICATION NUMBER: 60/145698
OR APPLICATION NUMBER: 60/14622
OR FILING DATE: 1999-07-28
OR APPLICATION NUMBER: 60/146963
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APPLICATION NUMBER: 60/169495
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APPLICATION NUMBER: 60/169835
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FILING DATE: 1999-11-09
APPLICATION NUMBER: 60/166361
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APPLICATION NUMBER: 60/169445
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APPLICATION NUMBER: 60/131445
FILING DATE: 1999-04-28
APPLICATION NUMBER: 60/134287
FILING DATE: 1999-05-14
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FILING DATE: 1999-04-26
APPLICATION NUMBER: 60/131270
FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131291
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FILING DATE:
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FILING DATE: 1999-04-21
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  ALRCAVKESKFWSDWSQEKMGMTEEEAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: 60/151733
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RESULT 12
US-10-219-076-92
US-10-219-076-92
Sequence 92, Application US/10219076
Publication No. US20030078379A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

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RESULT 13
US-10-230-434-92
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LENGTH: 582
                                                                    Sequence 92, Application US/10230434 Publication No. US20030078380A1 GENERAL INFORMATION:
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ORGANISM: Homo Sapien
-10-219-076-92
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                                  APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc
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PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
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ENT APPLICATION NUMBER: US/10/219,076
ENT FILING DATE: 2002-08-14
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APPLICATION NUMBER: 60/062287
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/063549
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079294
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Desnoyers, Luc
Gerritsen, Mary
Goddard, Audrey
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Goddard, Audrey
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Grimaldi, J. Christopher
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CURRENT APPLICATION NUMBER: US/10/230,434
CURRENT FILING DATE: 2002-08-28
CURRENT FILING NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 10/119,480
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/059113
FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
FILING DATE: 1998-08-17
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APPLICATION NUMBER: 60/095916
FILING DATE: 1998-08-10
APPLICATION NUMBER: 60/096146
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/095302
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/086392
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APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/095318
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APPLICATION NUMBER: 60/089532
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OR APPLICATION NUMBER: 60/131445
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OR FILING DATE: 1999-05-14
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RESULT 14
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APPLICANT:
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PRIOR FILING DATE: 2002-04-09
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ITTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC PRICE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER:
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FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090691
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086392
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APPLICATION NUMBER: 60/082804
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Smith, Victoria
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DATE: 1998-12-23

WARPLICATION NUMBER: 60/115558

DR FILING DATE: 1999-01-12

DR APPLICATION NUMBER: 60/115565

DR FILING DATE: 1999-01-12

DR APPLICATION NUMBER: 60/115733

DR FILING DATE: 1999-01-12

DR APPLICATION NUMBER: 60/119549
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DR APPLICATION NUMBER: 60/108849

DR FILING DATE: 1998-11-18

DR APPLICATION NUMBER: 60/112422

DR FILING DATE: 1998-12-15

DR APPLICATION NUMBER: 60/113296

DR FILING DATE: 1998-12-22

DR APPLICATION NUMBER: 60/113605
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APPLICATION NUMBER: 60/108787
FILING DATE: 1998-11-17
APPLICATION NUMBER: 60/108801
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APPLICATION NUMBER: 60/106248
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APPLICATION NUMBER: 60/106464
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APPLICATION NUMBER: 60/101922
FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/106178
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APPLICATION NUMBER: 60/101786
FILING DATE: 1998-09-25
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FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/101741
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APPLICATION NUMBER: 60/101477
FILING DATE: 1998-09-23
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APPLICATION NUMBER: 60/100390
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APPLICATION NUMBER: 60/100627
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099816
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APPLICATION NUMBER: 60/099803
FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099596
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099598
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FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
FILING DATE: 1998-08-17
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APPLICATION NUMBER: 60/106905
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APPLICATION NUMBER: 60/098544
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APPLICATION NUMBER: 60/113621
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FILING DATE: 1999-03-23
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Similarity 100.0%; Pred. No. 4.6e-104;
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                 ALRCAVKESKFWSDWSQEKMGMTEEEAP
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Matches 208
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APPLICANT: Desnoye
APPLICANT: Gerrite
APPLICANT: Goddard
APPLICANT: Godows'
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Publication No.
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LENGTH: 582
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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR PRIOR APPLICATION NUMBER: 60/062287
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PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR APPLICATION NUMBER: 60/069873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WOOD, WIlliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION. ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C61
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TYPE: PRT
ORGANISM: Homo Sapien
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FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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                      ALRCAVKESKFWSDWSQEKMGMTEEEAP 208
                                                                             IQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J. Christopher
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No. US20030088064A1
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Gerritsen, Mary
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OM protein - protein search, using sw model
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                                                            August 18, 2003, 13:23:02; Search time 29.1496 Seconds (without alignments) 686.221 Million cell updates/sec
US-09-892-949-2_COPY_20_227
1121
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Title:
Perfect score:
Sequence:

1 ALPAKPENISCVYYYRKNLT.....SKFWSDWSQEKMGMTEEEAP 208

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues

Searched:

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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348	432	422	372	630	1092	372	837	1097	622	376	288	863	783	771	616	831	610	610	.412	310	581	830	809	303	292	918	918	917	Length	
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common cytokine re	interleukin-11 rec	interleukin-11 rec	ciliary neurotroph	prolactin receptor	differentiation-st	ciliary neurotroph	granulocyte colony			prolactin receptor		granulocyte colony	granulocyte colony	granulocyte colony			~							prolactin receptor	prolactin receptor	interleukin-6 sign	membrane glycoprot	copro	Description	

RESULT 2 A36337

membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 28-Jul-2000

5 10.0 531 4 820900	100	638 2 S12136	608 2 S32823	10.3 897 1 A39255	10.3 896 1 A35782	10.4 460 2 JL0145 i	440 2 JL0144 i	117.5 10.5 1162 2 PC4184 1	117.5 10.5 638 2 B28176 80	10.7 26926 1 138344	121 10.8 878 1 A40091 i	121.5 10.8 468 1 A41242 i	122.5 10.9 426 2 JC7773 I	124 11.1 1825 2 T32828 h	124 11.1 1825 2 C88400	Stowers Stowers
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# ALIGNMENTS

RESULT 1 149699

4515.1; PID:g840817  Length 917;  Indels 15; Gaps 9;  GEKHDNCTTNSSTSENRAS 61                         KTEPPKIFRVKPULGIKRM 120                         TKPTPPYNLSVTNSEBLSSI 237  DKNOTYNLTGLOPFTEYVI 180  SPRTSFTVQDLKPFTEYVF 295	62 180 121 238	?
61	62 180	B 8
61		B 8
	7 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYAFGEKHDNCTTNSSTSENRAS 61	B 8
.1; PID:9840817	Query Match 24.2%; Score 271.5; DB 2; Length Best Local Similarity 31.4%; Pred. No. 2.3e-15; Matches 66; Conservative 45; Mismatches 84; Indels	Z W O
.1; PID:g840817	A;Gene: gp130 A;Gene: gp130 C;Superfamily: cytokine receptor homology C;Keywords: glycoprotein F;134-314/Domain: cytokine receptor homology <crs></crs>	F C C A C
	A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-917 <re2> A;Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817 C:Genetics:</re2>	8 K K K C C
, PID:g193592	A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mXNA A;Residues: 1-917 <res> A;Cross-references: GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592 A;Accession: I48370</res>	A A A A A A C R M S
ange 28-Jul-2000 ated signal transducer, gp13	glycoprotein 130 - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000 C;Accession: I4969; I48370 R;Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T. J. Immunol. 148, 4066-4071, 1992 J. Immunol. 148, 4066-4071, 1992 A;Title: Molecular cloning of a murine IL-6 receptor-associated signal tran A;Reference number: I48370; MUID:92291532; PMID:1602143 A;Accession: I49699	A P S S S S S S S S S S S S S S S S S S

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Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an II-6 signal A;Reference number: A36337; MUID:91084844; PMID:2261637 A;Recession: A36337
                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBI C;Superfamily: cytokine receptor homology C;Keywords: transmembrane protein F;134-315/Domain: cytokine receptor homology <CRS>
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A;Molecule type: mRNA
A;Residues: 1-918 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-6 signal transducing molecule gp130 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
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C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>
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C;Genetics:
C;Genetics: GP130
A;Cross-references: GDB:126725; OMIM:600694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.;
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Residues: 1-918 <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YST-----VYFV-----NIEVWVEAENALGKVTSDHINFDPVYKV-KPNPPHNLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVK---RTYAFGE---KHD---NCTIN
                IQIEWIKDELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI
                                                                                                                                                    PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYAFGEKHDNCTTNSSTSENRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSTSENRASCSFFLPRITIPDNYTIEVEAENGDGVIKS-HMTYWRLENIAKTEPPKIFRV
                                                  CMMGYTPIYFV--NIEVWVEAENALGNVSSEPINFDPVDKVKPSPPHNLSVTNSEELSSI
                                                                                  CSF-FLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120
                                                                                                                      PDIPTNLSCIVNEGKNMLCQLDPGRETYLETNYTLKSEWA-TEKFPDCRTKHGTS----S
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Pred. No. 4.1e-15;
Pred. No. 4.7. Mismatches 76;
                                                                                                                                                                                                        Score 250; DB 2;
Pred. No. 1.6e-13;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fuller,
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                                                                                                                                                                                                                      Length 918;
                                                                                                                                                                                        Indels
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prolactin receptor precursor - mouse C;Species: Mus musculus (house mouse C;Date: 02-Aug-1996 #sequence revision)
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C;Date: 02-Aug-1996:
C;Accession: 177525
                                                                                                                                                                                                                                        A;Cross-references: GB:M22958; NID:g200479; PIDN:AAA39976.1; C;Superfamily: cytokine receptor homology
                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-303 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                              R; Davis, J.A.; Linzer, D.I.H. Mol. Endocrinol. 3, 674-680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M22959; NID:g200481; C;Superfamily: cytokine receptor homology
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A; Residues: 1-292 < RES>
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Mol. Endocrinol. 3, 674-680, 1989
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C;Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                     A;Reference number:
                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Expression
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Best Local &
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                                                                                                                               57;
                                                                                    3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
                                                                                                                                                    Similarity
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ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI
                                           PGKPEIHKCRSPDKETFTCWWNPGSDGGLPTNYSL--TYSKEGEKNTYECPDYKTSGPN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVBPEPPRNLTLEVKQLKDK 138
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of multiple forms of the prolactin
157699; MUID:89261824; PMID:2725531
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                                                                                                                          17.0%; Score 191; DB 2;
27.8%; Pred. No. 4.9e-09;
ive '38; Mismatches 92
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Pred. No. 4.7e-09;
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                                                                                                                                                                                                                      <CRS>
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                                                                                                                                                                      Length 303;
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A;Molecule type: mRNA
A;Residues: 1-557, 'F',559-608 <EDE>
A;Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
C;Comment: Prolactin receptor have long form and short form which are resul
C;Comment: This long form receptor is capable of transducing a signal to mi
C;Superfamily: cytokine receptor homology
C;Keywords: receptor; transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
F;330-253/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prolactin receptor, long form - mouse C;Species: Mus musculus (house newision 02-Aug-1996 #sequence revision 02-Aug-1996 C;Accession: I53269; JT0671; 334356
  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L13593; NID:g347398; PIDN:AAC37641.1; PID:g347842 R;Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A. submitted to the EMBL Data Library, June 1993 A;Description: Isolation and nucleotide sequence of a mouse cDNA prolact. A;Reference number: S34356
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A; Residues: 1-608 < MOO>
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A;Title: Changes in prolactin receptor expression during
A;Reference number: I53269; MUID:93307149; PMID:8319571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Clarke, D.L.;
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Best Local S
Matches 57
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                                                                                                                            FTEYVIALRCAVKESKFWSDWSQEK 199
                                                                                                                                                                                                                                                                                                   ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI 117
                                                                                                                                                                                                                                                                                                                                                                                         PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTYLWVKWLPPTITDVKTGWFTMEYEIRLKSEEADEW-EIHFTGHQTQ----FKVFDLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRMIQIEWIKPELAPVSS---DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTLEVKQLKDK
                                                                                                                                                                       KTYLWVKWLPPTITDVKTGWFTMEYEIRLKSEEADEW-EIHFTGHQTQ----FKVFDLYP
                                                                                                                                                                                                             KRMIQIEWIKPELAPVSS----DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQP 174
                                                                                                                                                                                                                                                                                                                                                 PGKPEIHKCRSPDKETFTCWWNPGSDGGLPTNYSL--TYSKEGEKNTYECPDYKTSGPN-
                                                                                                                                                                                                                                                        -SCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTLEVKQLKDK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linzer, D.I.H
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  17.0%; Score 191; DB 2; 27.8%; Pred. No. 1.2e-08; tive 38; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
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to milk protein ge
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A; Residues: 1-581 <SCO>
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A; Accession: I50455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I45971
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Best Local
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143
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RKPYLWIK-----WSPPTMTDVKSGWFIIQYEIRLKPEKATDW-ETHFTL----
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prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
C;Accession: I50455
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PRLR
C;Superfamily: cytokine receptor homology
F;36-221/Domain: cytokine receptor homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C;Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endocrinology 135, 269-276, 1994
A; Title: Cloning, expression, and mutational analysis A; Reference number: I50455; MUID:94283267; PMID:751686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor
A;Reference number: I45971; MUID:93246019; PMID:1338725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;240-426/Domain: cytokine receptor homology <CRS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L02549; NID:g163617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 TEYVIALRCAVKESKFWSDWSQEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 MIQIEWIKPELAPVSS---DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQT-YNLTGLQPF 175
                                                                                                                                                    59 RASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRV-----
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                                                                                                                                                                                                                                                         3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTY-AFGEK--HDNCTTNSSTSEN
                                                                                                --SCYFSKKHTSIWKMYVITVNAINQMGISSSDPLYVHVTYIVEPEPPANLTLELKHPED 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKYIVQIHCKPDHHGSWSEWSLEK
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                                           -KPVLGIKRMIQIEWIKPELAPVSSD---LKYTLRFRTVNSTSWMEVNFAKNRKDKNQTY 167
                                                                                                                                                                                                        PEKPKLVKCRSPGKETFTCWWEPGADGGLPTNYTL--TYHKEGETLIHE-CPDYKTGGPN
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27.9%; Pred
27;
                                                                                                                                                                                                                                                                                                                                   16.3%; Score 183; DB 2;
28.9%; Pred. No. 5.4e-08;
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Pred. No. 1.9e-08;
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                                                                                                                                                                                                                                                                                                                                                            Length 581;
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KQTQL 191
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A;Cross-references: GB:M74152; NID:g206389; PIDN:AAA419
R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A;Title: Differential signal transduction of the short,
A;Reference number: I55417; MUID:95014432; PMID:7929319
                                                                                                                                                                                                                                                                                   R;Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A;Title: A prolactin-dependent immune cell line (Nb2) e.
A;Reference number: A41070; MUID:92041834; PMID:1718958
A;Accession: A41070
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A41070
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A;Title: Cloning and expression of the rat prolactin receptor, A;Reference number: A29884; MUID:88165059; PMID:2832068
A;Accession: A29884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30
C;Accession: A29884
0022
                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-412 < ALI>
                                                                                                                                                                                                                                                                                                                                                                                            prolactin receptor Nb2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Un-1992 #sequence revision 12
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             ;Molecule type: mRNA;Residues: 1-412 <RES>,

;Residues: 1-412 <RES>,

;Cross-references: EMBL:U07567; NID:g641963;

;Experimental source: NB2-11C cell line;

;Superfamily: cytokine receptor homology
Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;1-19/Domain: signal sequence #status predicted <SIG>;20-310/Product: prolactin receptor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   Accession: A41070; I55417
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Best Local
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57; Conserv
 transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTEYVIALRCAVKESKFWSDWSQE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEW-EIHFTGHQTQ----FKVFDLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRMIQIEWIKPELAPVSS---DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSL--TYSKEGEKTTYECPDYKTSGPN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SCFFSKQYTSIWKIYIITVNATNOMGSSSSDPLYVDVTYIVEPEPPRNLTLEVKQLKDK 138
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cytokine receptor homology <CRS>
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procein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 181; DB 2;
Pred. No. 3.7e-08;
5; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                    12-Jun-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
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                                                                                                                                                                                                                            PIDN: AAA41946.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:AAA41937.1; PID:g206365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                       PIDN: AAA61784.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 310;
                                                                                                                                                                                                                                                                                                                       expresses
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C; Decino.
C; Date: 13-Jul-1990 #sequence_revible.
C; Date: 13-Jul-1990 #sequence_revible.
C; Accession: A34631
R; Zhang, R.; Buczko, B.; Tsai-Morris, C.H.; Hu, Z.Z.; Duff, Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A; Title: Isolation and characterization of two novel rates of two novel ra
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A34631
                                                                                                                        prolactin receptor 2 precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Mar-1991 #sequence_revision 28 C;Accession: A36116
                                                          R;Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, Mol. Endocrinol. 4, 1136-1143, 1990
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A;Note: the authors translated the codon GAg for residue 533
C;Superfamily: cytokine receptor homology
F;31-216/Domain: cytokine receptor homology <CRS>
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A; Residues: 1-610 < ZHA>
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A; Accession: A34631
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A; Reference number:
                                A; Title: Expression
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-Jul-1990 #sequence_revision 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FTEYVIALRCAVKESKFWSDWSQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSL--TYSKEGEKTTYECPDYKTSGPN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEW-EIHFTGHQTQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPPRNLTLEVKQLKDK 138
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forms of prolactin; MUID:91155946; PMI
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tin receptor in PMID:2293022
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1990
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                                                                                           C.; Boutin, J.M.; Edery, M.;
                                                                                                                                                     #text_change 28-Jul-2000
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C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: kidney
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M57668; NID:g206366; PIDN:AAA41938.1; PID:g206367; C;Superfamily: cytokine receptor homology F;31-216/Domain: cytokine receptor homology <CRS>
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <SHI>
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C;Species: Gallus gallus (chicken)
C;Date: 30-Sep_1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                              ;239-425/Domain: cytokine receptor homology <CRS2>;439-462/Domain: transmembrane #status predicted <TMM>;59,91,100,112,132,262,303,315,335,647,701,800/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;36-219/Domain: cytokine receptor homology <CRS1>
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Best Local
                                         177
                                                                                 349
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  404
                                                                                                                      120 MIQIEWIKPELAPVSS----DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFT 176
                                                                                                                                                                289 CYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKPINRKP
                                                                                                                                                                                                      62 CSFFLPRITIPDNYTIEVBAENGDGVIKSHMTYWRLENIAKTEPP--KIFRVKPVLGIKR
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                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                       3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYAFGEKHDNCTTNSSTSENRAS
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                                   EYVIALRCAVKESKFWSDWSQE 198
                                                                             YLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
KYIIQIHCKPDHHGSWSEWSSE
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26.7%;
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                                                                                                                                                                                                                                                                                                                                   26;
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R;Fukunaga, R.; Seto, Y.; Mizushima, S.; Negata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A;Tille: Three different mRNAs encoding human granulocyte
A;Reference number: A38252; MUID:91062348; PMID:1701053
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A;Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167,A;Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167,A;Residues: 41-58,'X',60-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-97,00-66;90-
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A;Title: Identification and sequence analysis of a second form of prolactin A;Reference number: A30304; MUID:89184578; PMID:2928321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocyte colony-stimulating factor receptor precursor (clone pHQ2) - human C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 05-Nov-1999
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                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-771 <FUK>
A;Cross-references: GB:M59819; GB:M38026; NID:g485363; PIDN:AAA63177.1;
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                                                                                                                                                                                                                                                                                                               Status:
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                                                                                                              Query Match
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                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTY-AFGE--KHDNCTTNSSTSEN
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                                                                         14.8%; Score 166; DB 2; 27.1%; Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
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Pred. No. 9.4e-07;
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                                         96;
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                                                                                                          Length 771;
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                                    54;
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Search completed: August 18, 2003, 13:31:21 Job time : 30.1496 secs	282 VGPLPLEALQYELCGLLPATAYTLQIRCIRWPLPGHWSDWSPSLELRTTERAP 334	154 VNFAKNRKDKNQTYNLTGLQPFTEYVIALRC-AVKESKFWSDWSQEKMGMTEEEAP 208	235 MDPSPEAAPPQAGCLQLCWEPWQPGLHINQKCELRHKPQRGEASWAL 281	111 VKPVLGIKRMIQIEWIKPELAPVSS	175 LDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRT 234	56SENRASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFR 110	123 PAIPHNLSCLMNLTTSSLICQWEPGPETHLPTSFTLKSFKSRGNCQTQGDSI 174	YYRKNLT(

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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34
107	107.5	108.5	109	109.5	110.5	111.5	112	112	112.5	113.5	114
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	EMBL; X62646; CAA44515.1; EMBL; M83336; AAA37723.1; PIR; I49699; I49699. HSSP, P40189; 1BQU. MGD; MGI:96560; I16st. GO; GO:0007165; P:signal transduction; InterPro; IPR002996; CRIA.	modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).	use by non-profit institutions as long	-!- SIMILARITY: Contai	-!- DEVELOPMENTAL 6 OF GESTATIO	-!- SUBCELLULAR L -!- TISSUE SPECIF SPLEEN, KIDNE EXCEPT BAF-BO	-	IL-6, LIF, OS SIGNAL TRANSM	transducer, gp130, and its regul J. Immunol. 148:4066-4071(1992).	MEDLINE-92291532; PubMed=1602143; Saito M., Yoshida K., Hibi M., Ta "Molecular cloning of a murine IL	SEQUENCE FROM N.A. STRAIN=ICR; TISSUE=Macrophage;	Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;	Mus musculus (Mouse) Eukarvota: Metazoa:	Interleukin-6 receptor beta chain precursor (IL-6R-beta) 6 signal transducer) (Membrane glycoprotein 130) (GP130) 11,637	01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update	Q00560; 01-FEB-1995 (Rel.	RESULT 1 IL6B_MOUSE ST
	46; CAA44515.1; 36; AAA37723.1; 9; I19699. 89; IBQU. 6560; I16st. 7165; P:signal transd. IPR002996; CRIA.	statement is a license agrito license@isb	s wiss-ract entry is copyright. It ween the Swiss Institute of Bioinformatics Institute. Buropean Bioinformatics Institute. by non-profit institutions as lo	ontains 1 immu ontains 5 fibr ELONGS TO THE	STAGE: IN EMB	SUBCELLULAR LOCATION: Type I TISSUE SPECIFICITY: FOUND IN SPLEEN, KIDNEY, LUNG AND LIVI EXCEPT BAF-B03. EXPRESSION N	AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MA EMBRYONIC DEVELOPMENT. SUBUNIT: Heterodimer of an alpha and a beta chain	MAL-TRANSDUCING M, CNTF, AND IT ISSION. BINDS	, and its regu 066-4071(1992)	PubMed=160214 K., Hibi M., ' G of a murine	E=Macrophage;		se). a; Chordata; C	eptor beta cha er) (Membrane (	31, Last seque	31, Created)	ANDARD; P
	uction; IDA:	not removed. eement (See h esib.ch).	gnt. It is pr Bioinformati titute. Ther ns as long a	noglobulin-li onectin type CYTOKINE FAMI	RYONIC STEM C A PEAK ON DAY	I membrane pr N TISSUES SUC VER. FOUND IN	DOES NOT BIND	G MOLECULE. T L-11 CAN UTIL TO IL-6/IL-6-	lated express	3; Taga T., Kish IL-6 receptor		Sciurognathi; Muridae;	raniata; Vert	in precursor glycoprotein	Last sequence update) Last annotation update)		RT; 917 AA.
•	ŝn, ≉	is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce	the the conte	SIMILARITY: Contains 1 immunoglobulin-like C2-type domain. SIMILARITY: Contains 5 fibronectin type III domains. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CÉLLS IT IS FOUND F 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY D DIDING THE BEST OF EMBRYOGENESIS	SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE	AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE EMBRYONIC DEVELOPMENT. SIMUNIT: Heterodimer of an alpha and a beta chain.	FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE REPLET OF INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, DEGITATING IN THE PORPHATION OF HIGH APERATTY IL-6 BINDING SITTED	and its regulated expression in vivo.";  66-4071(1992).	MEDLINE-92291532; PubMed=1602143; Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.; "Molecular cloning of a murine IL-6 receptor-associated signal		Murinae;	ebrata: Euteleostomi:	•			
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Q14627 Q62959

homo sapien

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P40189; Q9UQ41;

f 01-FEB-1995 (Rel. 31, Created)

T 01-FEB-1995 (Rel. 31, Last sequence update)

JT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Interleukin-6 receptor beta chain precursor (ILDE 6 signal transducer) (Membrane glycoprotein 130 receptor) (CDw130) (CD130 antigen).
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Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 5
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Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
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EMBL; M57230; AAA59155.1; -.
EMBL; AB015706; BAA78112.1; -.
FIR; A36337, A36337.
PDB; 1EQU; 26-AUG-98.
PDB; 1BJB; 13-JAN-99.
PDB; 1IR; 28-MAR-01.
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Bravo J., Staunton D., Heath J.K., Jones "Crystal structure of a cytokine-binding EMBO J. 17:1655-1674 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              examined. Expression not restricted to IL-6 responsive cells.

- IDISBASE: Isoform 2 is an autoantigen found in rheumatoid arth (RA) but it is not specific to patients with RA.
- I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
- ISIMILARITY: Contains 5 fibronectin type III domains.
- I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
- I- DATABASE: NAME-PROW; NOTE-CD guide CD130 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakami M., Nakao K.;
Murakami M., Nakao K.;
"Cloning of novel soluble gp130 and detection
autoantibodies in rheumatoid arthritis.";
J. Clin. Invest. 106:137-144(2000).
MIM; 600694; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004898; F:gpl30; TAS.
GO; GO:0004924; F:oncostatin-M receptor activity; TAS
GO; GO:0004872; F:receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=GP130-RAPS;
IsoId=P40189-2; Sequence=VSP_001684, VSP_001685;
-!- TISSUE SPECIFICITY: Found in all the tissues and cell lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91084844; PubMed=2261637;
Hibi M., Murakami M., Saito M., H
"Molecular cloning and expression
gpi30.";
Cell 63:1149-1157(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20341529; PubMed=10880057;
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SUBUNIT: Heterodimer of an alpha and a beta chain.
SUBCELLULAR LOCATION: Type I membrane protein (1sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Signal-transducing molecule. The receptor systems for IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for initiating signal transmission. Binds to IL-6/IL-6-R (alpha chain) complex, resulting in the formation of high-affinity IL-6 binding sites, and transduces the signal Does not bind IL-6. May have a sites, and transduces the signal of the signal bind IL-6.
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InterPro; IPR003961; F
InterPro; IPR003529; H
Pfam; PF00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                          TURN
                                                                              HELIX
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01353; HEMATOPO REC L F2; 1.
Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                   STRAND
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GO:0006955;
                                                                                                                                                                                                                                                                                                                                                                  3D-structure;
                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Gryuce
Transmembrane; Gryuce
                 918
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138
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139
147
164
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168
24.0%;
30.3%;
                103522 MW;
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N-LINKED
N-LINKED
N-LINKED
Score 268.5; DB Pred. No. 3e-17;
                                                                                                                                                                                          Missing (T
                                                                                                                                                                                                                                                                                                                                           INTERLEUKIN-6 RECEPTOR BE EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                N-LINKED
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                                                                                                                                                                                                    FTId=VSP
                D813F3672DD10D53 CRC64;
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                                                                                                                                                                                                       (GLCNAC . . ) . (GLCNAC . . ) .
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(in isoform
                                                                                                                                                                                                                                                      (GLCNAC. .
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TYPE-III
TYPE-III
TYPE-III
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     Length 918;
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11.6B RAT
1D 11.6B RAT
AC P40150;
DT 01-FEB-1995
DT 01-FEB-1995
DT 16-OCT-2001
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                                     EMBL; M92340; -; NOT_ANNOTATED_CDS
PIR; A44257; A44257.
HSSP; P40189; 1BQU.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
    SMART; SM00060; F
PROSITE; PS01353;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Liver;
                Pfam; PF00041; fn3; 3.
                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                               STANDARD;
          FN3;
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                                                                                                                                                                                                                                                                                               PRT;
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-!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING CONTRACTION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BIDDING SITES, CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).

CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.

CC -!- SUBUNITAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS AND EXDOTHELIAL CELLS.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FBB-1995 (Rel. 31, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Interleukin-6 receptor beta chain precursor (IL-6R-beta)
6 signal transducer) (Membrane glycoprotein 130) (GP130)
IL6ST.
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93052397; PubMed=1427893; Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.; Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.; "Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule, gp130."; Genomics 14:666-672(1992).

-i- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
                                                                                                                    InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hemtopoptn_L_F2
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P801353; HEMATOPO REC_L_F2; 1.
Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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6 outstation -
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Best Local :
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Q08501; P15212; P15213; Q
01-APR-1990 (Rel. 14, Cre
01-FEB-1995 (Rel. 31, Las
28-FEB-2003 (Rel. 41, Las
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DOMAIN
MEDLINE=94085788; PubMed=8262385;

Moore R.C., Oka T.;

"Cloning and sequencing of the cDNA encoding the long-form prolactin receptor.";

Gene 134:263-265(1993).
                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
MCI TaxID=10090;
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                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                       PRLR.
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918
                                                                                                                                                                                                                                 212; P15213; Q62099;
(Rel. 14, Created)
(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
eceptor precursor (PRL-R).
                                                                       TISSUE=Mammary gland;
85788; PubMed=8262385;
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
                                                                                                         PRL-R3).
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By similarity.
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By similarity.
By similarity.
N-LINKED (GLCNA)
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INTERLEUKIN-6
EXTRACELLULAR
POTENTIAL.
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Pred. No. 1
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                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                               PRT;
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les 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 918;
                                     murine mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                              Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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 EMBL; L1359; AAC37641.1; EMBL; L1359; AAC37666.1; EMBL; L14811; AAA02686.1; EMBL; D10214; BAA01066.1; EMBL; X73372; CAA51789.1; EMBL; M22959; AAA39977.1; EMBL; M22959; AAA39976.1; EMBL; M22958; AAA39976.1; EMBL; M25269; I33269. EMBL; M25269; I33269. EMBL; M25269; I33269. EMBL; M25269; I33269. EMBL; M25269; I37524. EMBL; M25269; I375269. EMBL; M25269; I375269. EMBL; M25269; I375269. EMBL; M25269; I375269. EMBL; M25269; 
DOMAIN
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STRAIN=BALB/c; TISSUE=Mammary gland;
Edery M., Pezet A., Nandi S., Kelly P.A.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A. (ISOFORM PRI-R3).
STRAIN=Swies Webster; TISSUS-Liver;
MEDLINE=93307149; PubMed=8319571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS PRL-R2 STRAIN=Swiss Webster; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Sasaki M.;
                                                                                                           SIGNAL
                                                                                                                            Receptor; T
Alternative
                                                                                                                                                              SMART; SM00060; FI PROSITE; PS01352;
                                                                                                                                                                                                  Pfam; PF00041; fn3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clarke D.L., Linzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression of multiple forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89261824; PubMed=2725531; Davis J.A., Linzer D.I.H.;
                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                            MGI:97763; Prlr.
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                                                                                                                                                                                                                                                                                       177525; 177525.
P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q08501-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q08501-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q08501-1;
                                                                                                                                                                                                                IPR002996; CR1A.
IPR003961; FN_III.
IPR003528; Hemtopoptn_L_F1.
                                                                                                                                               Transmembrane;
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 FIBRONECTIN
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as gas its cont
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Changes in prolactin receptor expression during pregnancy in the mouse ovary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPT
-!- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II. SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;
                 POTENTIAL.

PROLACTIN RECEPTOR.

EXTRACELLULAR (BY SI
BY SIMILARITY.

CYTOPLASMIC (BY SIMI
FIBRONECTIN TYPE-III
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                              Signal; Repeat;
C (BY SIMILARITY).
N TYPE-III 1.
N TYPE-III 2.
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SEQUENCE
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VARSPLIC
                 This SWISS-PROT entry is copyright. It is prod between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                TISSUE=Cropsac;
MEDLINE=94283267; PubMed=7516866;
Chen X., Horseman N.D.;
                                                                                                                                                                                                                               Columba livia (Domestic pigeon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Ayes; Neognathae; Columbiformes; Columbidae; Columba
 entities requires a license or send an email to license
                                                                                                                           Endocrinology 135:269-276(1994).
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    -!- SUBCELLULAR LOCATION: Type I membrane protein.
    -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
    -!- SIMILARITY: Contains 4 fibronectin type III domains.

                                                                                                                                                receptor.";
                                                                                                                                                           "Cloning,
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=8932;
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                                     yright. It is produced through a collab
of Bioinformatics and the EMBL outst
Institute. There are no restrictions
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Pred. No. 3.2e-10;
8; Mismatches 92;
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/FTId=VSP_
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KGKSEBLLSALGCQDFPPTSDCE_-> LWCSILQLTSLVKI
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                                        NCBI_TaxID=9860;
                                                                                                     01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
MEDLINE=96030711; PubMed=7561644;
Clarke L.A., Edery M., Loudon A.S
                  TISSUE=Liver
                          SEQUENCE FROM N.A.
                                                                             Cervus elaphus (Red
                                                                                              Prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00041; fn3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150455; IS0455.
                                                                                                                                                                                                                    350
                                                                                                                                                                                                                                                       290
                                                                                                                                                                                                                                                                                        232
                                                                                                                                                                                   404
                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P16471; 1BP3
                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                    TLVLTWSPPPLADVRSGWLTLDYELRLKPEEABEWETIFVGQ----
                                                                                                                                                                                                                                                                                                         PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYAFGEKHDNCTTNSSTSENRAS
                                                                                                                                                                                                                                  MIQIEWIKPELAPVSS---DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQT-YNLTGLQFF
                                                 Eutheria;
Cervinae;
                                                                                                                                                                                   KKYIVQIHCKPDHHGSWSEWSLEK
                                                                                                                                                                                                   TEYVIALRCAVKESKFWSDWSQEK
                                                                                                                                                                                                                                                      CYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNRKP
                                                                                                                                                                                                                                                                      CSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPP--KIFRVKPVLGIKR
                                                                                                                                                                                                                                                                                       PEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTLLYSKEGEERVYECPDYKTAGPN--S
                                                                                             receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002996; CR1A.
IPR003961; FN_III.
                                                                                                    (Rel. 35, (Rel. 35, (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA20646.1;
                                                                                                                                                                                                                                                                                                                                                             AA,
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEMATOPO
                                                                                                                                                                                                                                                                                                                                                                     112
1132
132
304
316
                                                                                             precursor
                                                    Cervus
                                                           Chordata; Crania
Cetartiodactyla;
                                                                             deer)
                                                                                                                                                                                                                                                                                                                                                             94507
                                                                                                                                                                                                                                                                                                                                  17.0%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hemtopoptn_L_F1
                                                                                                    Last sequence update)
Last annotation update)
Loudon A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                             ¥,
                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
FIBRONECTIN 'FIBRONECTIN'
                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                              (PRL-R).
                                                                                                                                                                                                                                                                                                                          Score 190.5; DB
Pred. No. 5.3e-10
7; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. 3B074E83CDF69EFF
                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLACTIN RECEPTOR
                                                           Craniata; Vertebrat
actyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                       PRT;
                                                                                                                                                                                   427
                                                                                                                                                                                                    199
Randall V.A.,
                                                                                                                                         581
                                                                                                                                                                                                                                                                                                                                                                   GECNAC
GECNAC
GECNAC
GECNAC
GECNAC
GECNAC
GECNAC
GECNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Repeat
                                                           Vertebrata; Eute minantia; Pecora;
                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                   .3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                           105;
                                                                                                                                                                                                                                                                                                                                           ۲,
                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4001
Postel-Vinay M.C.,
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                     Euteleostomi;
                                                                                                                                                                                                                    -QTHYKMFSLNPG
                                                            Cervoidea;
                                                                                                                                                                                                                                                                                                                                            830;
                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                     403
                                                                                                                                                                                                                                                      349
                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                        289
                                                                                                                                                                                                                                                                                                          61
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RESULT 7
PRIR SHEEP
ID PRIR S:
AC 046561
AC 046561
DT 28-FEB
DT 15-SEP
DE Prolac
GN PRIR.
OS Ovis a
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 63
                              PRLE SHEEP STANDARD; PR
046561; 046569; 046573; 046574;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last seque
15-SEP-2003 (Rel. 42, Last annot
                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelly P.A., Jabbour H.N.;
"Expression of the prolactin receptor gene during the breeding a non-breeding seasons in red deer (Cervus elaphus): evidence for expression of two forms in the testis.";
J. Endocrinol. 146:313-321(1995).
--- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS T
-!- SIMILARITY: Contains
                        Prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EW Buropean Bioinformatics Institute. There are no restr by non-profit institutions as long as its content fied and this statement is not removed. Usage by and
  aries
                                                                                                                                                           168
                                                                                                                                                                                 143
                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X94953; CAA64419.1;
P14787; IAN3.
                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                    59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00060; FN3;
                                                                                                                                                                                                                                                                                                                   . Similarity 63; Conser
                                                                                                                                                          NLTGLOPFTEYVIALRCAVKESKFWSDWSQE
                                                                                                                                     KIFSLYPGOKYLVOVRCK-PDHGYWSEWSPE
                                                                                                                                                                                                                             --TCYFSKKHTSIWKIYVITVNAINQMGVSSSDPLYVDVTYIVEPEPPANLTLELKHPED
                                                                                                                                                                                                                                                  RASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRV-----
                                                                                                                                                                                                                                                                        PGKPKI IKCRSPGKETFTCWWEPGSDGGLPTNYTL--TYHKEGETLIHE-CPDYKTGGPN
                                                                                                                                                                                                      -KPVLGIKRMIQIEWIKPELAPVSSD---LKYTLRFRTVNSTSWMEVNFAKNRKDKNQTY
                                                                                                                                                                                                                                                                                             PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTY-AFGEK--HDNCTTNSSTSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002996;
                                                                                                                                                                                                                                                                                                                                                               25
25
235
259
259
25
123
36
75
75
132
  (Sheep)
                                                                                                                                                                                                                                                                                                                  16.7%;
ilarity 29.9%;
Conservative 2:
                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                Ŋ,
                                                                                                                                                                                                                                                                                                                                                           24
581
234
258
558
1122
227
46
86
86
86
86
86
86
86
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMATOPO
                       precursor (PRL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FN_III.
Hemtopoptn_L_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR1A
                                                                                                                                                                                WFPPTLTDVKSGWFMIQYEIRLKPETAADW-EIHFAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N: Type I membrane protein.
TO THE CYTOKINE FAMILY OF RECEPT
s 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glyco
                                                                                                                                                                                                                                                                                                                                                                 ₹
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REC L
                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

CYTOPLASMIC (POTENTIAL FIBRONECTIN TYPE-III 1 FIBRONECTIN TYPE-III 1 FIBRONECTIN TYPE-III 2 FIBRONECTIN TYPE-III 2 BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                  Score 187; DB 1; Pred. No. 7.1e-10; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN RECEPTOR EXTRACELLULAR (POT
                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
                                                                   P79203; P79205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cein;
                                                                             581 AA.
                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Repeat.
                                                                                                                                                          198
                                                                                                                                     221
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      Length 581;
                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               2.1
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration MBL outstation -
                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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r the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ons on its
in no way
commercial
                                                                                                                                                                                KOTOL
                                                                                                                                                                                 191
                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                        84
   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                ++
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                     Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tortonese D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.
           Alternative
                                                                  InterPro;
                                                                                        InterPro;
                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
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S 맑 á 밁 Ś 밁 S

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EMBL; AF041257; AAB96795.1; --
EMBL; AF041977; AAB96920.1; --
EMBL; AF041979; AAB97082.1; --
EMBL; AF042358; AAB97744.1; --
EMBL; AF042358; AAB97743.1; --
EMBL; AF041978; AAB96965.1; --
EMBL; Y10578; CAA71597.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djian "Long and short forms of the ovine prolactin receptor: cDNA clonis and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."; J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a licence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Corpus luteum, and Fetal liver;
Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.,
"Two forms of the prolactin receptor messenger ribonucleic
present in ovine fetal liver and adult ovary.";
Endocrine 3:291-295(1995).
                                                                             SMART; SM00060; FN
PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: Expressed in all tissues examined; l pituitary, adrenal gland, ovary and fetal liver.
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Detection of prolactin receptor gene expression pituitary gland and visualization of the specific signal in gonadotrophs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver, and Mammary gland; MEDLINE=98001468; PubMed=9343303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrinology 139:5215-5223(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99049302; PubMed=9832462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Scottish blackface; TISSUE=Anterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event-Alternative splicing; Named isofc Name=1; Synonyms=Long, L-OPR; IsoId=046561-1; Sequence=Displayed; Name=2; Synonyms=Short, S-OPR; IsoId=046561-2; Sequence=VSP_001732,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prolactin.
SUBCELLULAR LOCATION: Type
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=3; Synonyms=Soluble;
IsoId=046561-3; Sequence=VSP_001730, VSP_001731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This is a receptor for the anterior pituitary hormone
                                                                                                                                 PF00041; fn3;
                                                                                                                                                                                                                                          P14787; 1AN3
                                                                                                                                                                                                                                                                Y10578; CAA71597.1; -.
Y10808; CAA71766.1; -.
                                                                                                                                                    IPR002996; CR1A.
IPR003961; FN_III.
IPR003528; Hemtopoptn_L_F1.
                                                    Transmembrane;
Faus...
a splicing.
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147-302 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61-395 FROM N.A., ALTERNATIVE SPLICING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brooks J. Ingleton P.M., McNeilly A.S.;
rolactin receptor gene expression in the sheep
                                                                                                           FN3;
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                                                                                HEMATOPO_REC_L_F1; 1
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                                                 Glycoprotein;
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                                                    Signal; Repeat;
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                         MEDLINE=97098510; PubMed=8943050; Presky D.H., Yang H., Minetti L.J., Gately M.K., Gubler U.;
                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Interleukin-12 receptor beta-2 chain precur
                                                                                                                    NCBI_TaxID=9606;
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16-OCT-2001
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                                                             "A functional interleukin 12 receptor
                                                                                                   SEQUENCE FROM N.A.
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      SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT
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N-LINKED (GLCNAC. . . .) (POTENTIAL).
GOSPPEKFKLIKCRSPGKETFTCWWEDGALDGGLPTNYTLTY
RK -> ASLYVPGGKCSSVCTYMAYPFVGGIFLHMYLCVDQ
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Catarrhini; Hominidae;
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-> V (IN REF. 1; AAB97743/AAB97744).
-> K (IN REF. 2).
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GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004907; F:interleukin receptor activity; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu.

GO; GO:0008284; P:positive regulation of cell proliferation; T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hemtopoptn_L_F2.
Pfam; PF00041; fn3; 3.
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HSSP; P40189;
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                                                                                                                                                                              177
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PFTEYEFQISSKLHLYKGSWSDWSESLRAQTPEEEP
                                          PFTEYVIALRCAVKESK-FWSDWSQEKMGMTEEEAP
                                                                                                                                 GIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNF--AKNRKDKNQTYNLTGLQ
                                                                                                                                                                              YCDYLDFGINLTPESPESNFTAKVTAVNSLGSSSSLPSTFTFLDIVRPLPPWDIRIKFQK
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CYTODIASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
N-LINKED (GLCNAC. .) (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -> V (IN dbsnp:2307146).
/FTId=VAR 014805.
G -> R (IN dbsnp:2307148).
/FTId=VAR 014806.
Q -> H (IN dbsnp:2307145).
                                                                                                                                                                                                                                                                                                                                                                                  Score 184;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    G -> D (IN dbSNP:2307153)
/FTId=VAR 014808. 67C0E0D946B8DD58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR 014807.
3 -> D (IN dbSNP:2307153)
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Repeat; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                          DВ
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RESULT 9
PRLR_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schuler L.A., Nagel R.J., Gao J., "Prolactin receptor heterogeneity tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q28172; 018880; 046591;
01-NOV-1997 (Rel. 35, C
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98001468; PubMed=9343303; Bignon C., Binart N., Ormandy C., S"Long and short forms of the ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tchelet A., Staten N.R., Creely D.P., Krivi G.G., Gertler A.; "Extracellular domain of prolactin receptor from bovine mammary gland: expression in Escherichia coli, purification and characterization of its interaction with lactogenic hormones."; J. Endocrinol. 144:393-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scott P., Kessler M.A., Schuler L.A.;
"Molecular cloning of the bovine prolactin receptor and
of prolactin and growth hormone receptor transcripts in
utero-placental tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prolactin receptor precursor (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRLR
                                                                                                                                 brain.
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
-i- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Mammary gland;
MEDLINE=95256770; PubMed=7738463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93246019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Endometrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Endocrinol. 89:47-58(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Endometrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                  IsoId=Q28172-2; Sequence=VSP_001718, VSP_001719; TISSUE SPECIFICITY: Expressed in all tissues examined; liver, peripheral blood lymphocytes, endometrium, corpus luteum, intestine, fetal thymus, fetal spleen, fetal liver and fetal
                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              taurus (Bovine).
                                                                                                                                                                                                                                                Name=Short
                                                                                                                                                                                                                                                                             Name=Long;
                                                                                                                                                                                                                                                                                             Event=Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9343303;
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PRIR RAT

ID PRIR RAT

STANDARD;

PRT;

610 AA.

1D PRIR RAT

AC P057IO; Q62832; Q63451; Q63479; Q63723; Q64274;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

Total receptor precursor (PRI-R) (Lactogen
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CARBOHYD
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DOMAIN
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EMBL; AF027403; AAB3999.1; --
EMBL; AF042780; AAB97748.1; --
EMBL; AF042780; AAB97747.1; ALT_SEO.
                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P14787; 1AN3.
        NCBI_TaxID=10116;
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                                                                                                                                                                              168 NLTGLOPFTEYVIALRCAVKESKFWSDWSQE
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                                                                                                                                                                                                                                                            59 RASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRV-----
                                                                                                                                                                                                                                                                                                                      61;
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                   RKPYLWIK--
                                                                                                                                                                                                                    -KPVLGIKRMIQIEWIKPELAPVSSD---LKYTLRFRTVNSTSWMEVNFAKNRKDKNQTY
                                                                                                                                                                                                                                        --SCYFSKKHTSIWKMYVITVNAINOMGISSSDPLYVHVTYIVEPEPPANLTLELKHPED
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IPR003961; FN_III.
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237
258
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122
227
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227
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237
                  Chordata;
Rodentia;
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                                                                                                                                                                                                  -WSPPTMTDVKSGWFIIQYEIRLKPEKATDW-ETHFTL----
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                                                                                                                                                                                                                                                                                                                       28;
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Missing (In isoform Shr
/FTId=VSP_001719.
H -> D (IN REF. 3).
E -> D (IN REF. 3).
L -> V (IN REF. 3).
E -> H (IN REF. 3).
E -> H (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                      Score 183; DB 1;
Pred. No. 1.7e-09;
8; Mismatches 90
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N-LINKED (GLCNAC. . .)
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BY SIMILARITY.
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                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                               7385C0D6956EE139 CRC64;
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                                                           receptor).
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                     Rattus
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TISSUE=Lymphoma;
MEDLINE=92041834; PubMed=1718958;
Ali S., Pelligrini I., Kelly P.A.;
"A prolactin-dependent immune cell line of prolactin receptor.";
J. Biol. Chem. 266:20110-20117(1991).
    EMBL;
EMBL;
EMBL;
EMBL;
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MEDLINE=91155946; PubMed=2293022;
Shirota M., Banville D., Ali S., Jolicoeur C.,
Edery M., Djiane J., Kelly P.A.;
"Expression of two forms of prolactin receptor"
                                                                                                                                entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Neal K.D., Yu-Lee L.Y.;
"Differential signal transduction of the short, Nb2, prolactin receptors. Activation of interferon regular cell proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 281-610 FROM N.A. Banville D., Stocco R., Murth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Ova
MEDLINE-90241201; PubMed-2159291;
Zhang R., Buczko E., Tsai-Morris
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                            modified
                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95014432; PubMed=7929319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang R., Buczko E., Tsai-Morris C.-H., "Isolation and characterization of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
                                                                                                                                                Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                   Name=4; Synonyms=NB2;
IsoId=P05710-4; Sequence=VSP_001729;
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=Short;
IsoId=P05710-2; Sequence=VSP_001725,
Name=3; Synonyms=Medium;
IsoId=P05710-3; Sequence=VSP_001727,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=Long;
IsoId=P05710-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4
  M57668;
M34083;
L48060;
U34730;
M19304;
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                                                                                                                                   an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D., Stocco R., Murthy K.K., Boie Y., (MAR-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                equires a license agreement (S email to license@isb-sib.ch).
; AAA41938.1; -.; AAA79273.1; -.; AAA79274.1; -.; AAA92053.1; -.; AAA41937.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269:26076-26082(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
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EMBL; U07567; AAA61784.1; -
PIR; A29884; A29884
PIR; A34631; A34631.
PIR; A36116; A36116.
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Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00041; fn3; 2.
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_F1.
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                                                                                                                                                                                                                                                                              Similarity
GOKYLVOTRCK-PDHGYWSRWSOE
                              FTEYVIALRCAVKESKFWSDWSQE
                                                                                                                                                                                                                            PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
                                                           KTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEBAEEW-BIHFTGHQTQ----FKVFDLYP
                                                                                            KRMIQIEWIKPELAPVSS----DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQP
                                                                                                                                                             ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI
                                                                                                                                                                                             PGKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSL--TYSKEGEKTTYECPDYKTSGPN-
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                                                                                                                                                                                                                                                             Score 181; DB Pred. No. 2.8e Pred. No. 2.8e
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N-LINKED (GLCNAC. . .)
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EXTRACELLULAR (BY SIMILARITY).
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/FTId=VSP_001727.
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V (IN REF. 2).
K (IN REF. 1).
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M (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the cDNA sequence.";
Biochem. Biophys. Res.
-!- FUNCTION: THIS IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D13154; BAA02439.1; -. PIR; JQ1655; JQ1655. HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=White leghorn; TISSUE=Kidr
MEDLINE=93075121; PubMed=1445292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01352; HEMATOPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka M., Maeda K., Okubo T., Nakash
"Double antenna structure of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLACTIN.

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: BELONGS TO THE CYTOXINE FAMILY OF RECEPTA

SIMILARITY: Contains 4 fibronectin type III domains.
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                                                                                        Similarity
PEKPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGEEQVYECPDYRTAGPN--
                                  PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYAFGEKHDNCTTNSSTSENRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
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29, Last sequence update)
36, Last annotation update)
r precursor (PRL-R) (CPRLP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PO_REC_L_F1; 1.
Glycoprotein; Signal;
                                                                                                                                             MW;
                                                                    Score 179.5;
Pred. No. 5.7e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
FIBROMECTIN TYPE-III 1.
FIBROMECTIN TYPE-III 2.
FIBROMECTIN TYPE-III 3.
FIBROMECTIN TYPE-III 4.
                                                                                                                                                             N-LINKED
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N-LINKED (GLCN
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                                                                                                                                               1C4E75791DCADBE9
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                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                (GLCNAC. .
                                                                      5.7e-09;
nes 109;
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                                                                                                       Length 831;
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EMBL; U22947; AAA75038.1; -.
EMBL; U22924; AAA75039.1; -.
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bloinformat
the European Bioinformatics Institute on
the by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                            Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
"Molecular cloning, tissue distribution, and expression of prolactin receptor during various reproductive states in gallopavo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O91094; Q91091; Q91092;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                 Pfam; PF00041; fn3; 4. SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Kidney;
MEDLINE=97057891; PubMed=8902221;
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NCBI_TaxID=9103;
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                                                                                                                   PROSITE; PS01352;
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                                                                                                                                                       IPR002996; CR1A.
IPR003961; FN_III.
IPR003528; Hemtopoptn_L_F1.
                                                                                                        Transmembrane;
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FIBRONECTIN TYPE
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                                                                              PROLACTIN
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; Galliformes; Meleagrididae; Meleagris.
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TYPE-III
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This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo the Buropean Bioinformatics Institute. use by non-profit institutions as lo modified and this statement is not remoentities requires a license agreement or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                       Presky D.H., Yang H.,
Gately M.K., Gubler U.
"A functional interled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                        beta-type cytokine receptor subunits.";
Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996)
-!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BIND
                                                                                                                                                                                                           MEDLINE=97098510; PubMed=8943050; Presky D.H., Yang H., Minetti L.J.,
                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-12 receptor beta-2 chain precurso
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                       functional interleukin 12 receptor complex
                                                                                                                                                                                                                                                                                                         (IL-12R-beta2).
                                                                              SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY
SIMILARITY: Contains 4 fibronectin type III domains.
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SUBUNIT: DISULFIDE-LINKED H
SAFFINITY IL-12 RECEPTOR IS
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Rodentia;
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Sciurognathi; Muridae;
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Best Local &
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P14787;
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SMART; SM00060; FN3;
PROSITE; PS01353; HEN
SEQUENCE FROM N.A.
TISSUE=Mammary gland;
MEDLINE=89184578; Pub
                                                                                                                                                                   01-APR-1990
28-FEB-2003
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                    TEYVIALRCAVKES - KFWSDWSQEKMGMTEEEAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002996; CR1A.
IPR003961; FN_III.
                                                               cepuccuniculus (Rabbit)
cuniculus (Rabbit)
cuniculus (Rabbit)
cuniculus (Rabbit)
cuniculus (Rabbit)
cuniculus (Rabbit)
cuniculus (Rabbit)
                                                                                                                                                               (Rel. 14, Created)
(Rel. 14, Last sequence up
(Rel. 41, Last annotation
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657
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436
534
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114
142
151
169
179
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                                                                                                                                                                                                                                    STANDARD;
   PubMed=2928321;
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                                                                                                                                                  precursor
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; Glycoprotein; S
OR 23 (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ME.
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N-LINKED (GLCNAC. ...
; 582E4D21BF1FBD67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.8e
1; Mismatches
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Pred. No. 1.
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CYTOPLASMIC
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INTERLEUKIN-12 RI
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
                                                                                                 Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the entitles requires a license agreement (See http://www.isb-siborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor.";
Proteins 27:459-468(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edery M., Jolicoeur C., Levi-Meyrueis C., Dusanter-Fourt I., Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.; Proteidou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.; Proteidou B., Boutin J.M., Lesueur B., Kelly P.A., Djiane J.; Petridou B., Boutin J.M., Lesueur B., Kelly P.A., Djiane J.; Petridou B., Boutin B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00060; FN3; PROSITE; PS01352; HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002996;
InterPro; IPR003961;
InterPro; IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1AN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halaby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Homology modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROLACTIN.

SUBCELLULAR LOCATION: Type I membrane protein.

SINILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPT
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A30304; A30304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J04510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D., Thoreau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                 AAA31457.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E., Djiane J., Morno of rabbit prolactin
 SI
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; FN_III.
; Hemtopoptn_L_F1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
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PROLACTIN RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHI
                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTERIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complexed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PITUITARY HORMONE
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(POTENTIAL).
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L outstation -
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RESULT 15
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Best Local
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                                                         SEQUENCE FROM N.A., GLN-440; HIS-510; HI Rieder M.J., Armel 7 Rajkumar N., Toth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCSR_HUMAN
Q99062;
                                                                                                                     MEDLINE=92091782; PubMed=1530796; Seto Y., Fukunaga R., Nagata S.; "Chromosomal gene organization of stimulating factor receptor."; J. Immunol. 148:259-266(1992).
                                                                                                                                                                                                                                                                                                                  Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosman Park L., Sorensen E., March C.J., Smith C.A., Estimulating "Expression cloning of a human granulocyte colony-stimulating receptor: a structural mosaic of hematopoietin receptor, immunoglobulin, and fibronectin domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
DOMAINS STRUCTURE.
MEDLINE=92007729;
Fukunaga R., Ishiz
                                                                                                                                                                                                       "Three diller.";
factor receptor.";
Acad. Sci.
                                                                                                                                                                                                                                            MEDLINE=91062348; PubMed=1701053; Fukunaga R., Seto Y., Mizushima S
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91079757; PubMed=2147944;
Larsen A., Davis T., Curtis B.M.,
Park L., Sorensen E., March C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CD114 antigen).
CSF3R OR GCSFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Granulocyte colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    TISSUE=Placenta;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                          SSUE=Placenta;
                                                                                                                                                                                                                                                                                                         Exp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTY-AFGE--KHDNCTTNSSTSEN
                                                                                                                                                                                                                                                                                                        Med. 172:1559-1570(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                 FROM N.A., AND VARIANTS THR-231; ASN-320; HIS-510; HIS-562 AND CYS-583.
                                              N., Toth E.i
1 (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RASCSFFLPRITIPDNYTIEVBAENGDGVIKSHMTYWRLENIAKTEPP---KIFRVKPVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGQKYLVQVRCK-PDHGFWSVWSPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEW-ETHFA----GQQTQFKILSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKRMIQIEWIKPELAPVSS----DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SCYFSKKHTSIWTIYIITVNATNOMGSSVSDPRYVDVTYIVEPDPPVNLTLEVKHPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGKPFIFKCRSPEKETFTCWWRPGADGGLPTNYTL--TYHKEGETITHE-CPDYKTGGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Ishizaka-Ikeda E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
             PubMed=1717255;
                                               T.Z., Carrington D.P., Ozu
E.J., Yi Q., Nickerson D.A.
2) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                                                                                                                                                                                                          Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
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29.3%;
                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                               Wizushima S., Ne encoding human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 169; DB
Pred. No. 3.7e
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                            87:8702-8706 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Pan
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                                                                                                                                                                                                                                              Nagata S.;
 C.-x.,
                                                                                                                                               human
                                                                                                                                                                                                                                 granulocyte
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                                                            D.A.;
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                                                                       Ozuna M.,
 Seto Y.,
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                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor (G-CSF-R)
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Dong F., Hoefsloot L.H., Schelen A.M., Broeders C.A., Meijer Y., Veerman A.J., Touw I.P., Lowenberg B.;
"Identification of a nonsense mutation in the granulocyte-colony-stimulating factor receptor in severe congenital neutropenia.";
Proc. Natl. Acad. Sci. U.S.A. 91:4480-4484(1994).
                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=4; Synonyms=GCSFR-4, D7;

IsoId=099062-4; Sequence=VSP 001671, VSP 001672;

IsoId=099062-4; Sequence=VSP 001671, VSP 001672;

IsoId=099062-4; Sequence=VSP 001671, VSP 001672;

WISIOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN MYSIOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELLS. IN BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES. THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

I-- DISEASE: Defects in CSF3R might be a cause of severe congenital neutropenia (SCN) in some patients.

I-- SIMILARITY: Contains 5 fibronectin type III domains.

I-- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

I-- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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MEDLINE=97331327; PubMed=9187659;

Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;

Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;

"Solution structure of an extracellular domain containing the motif of the granulocyte colony-stimulating factor receptor an interaction with ligand.";

Nat. Struct. Biol. 4:498-503(1997).
                                                                                                                                                                                                              entities requires or send an email t
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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MEDLINE=94240159; PubMed=7514305;
Hoefsloot L.H., Schelen A.M.,
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3D-STRUCTURE MODELING OF 125-331.
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EMBO J. 10:2855-2865(1991)
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receptor.";
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IsoId=Q99062-2; Sequence=VSP_001674;
Name=3; Synonyms=GCSFR-3;
IsoId=Q99062-3; Sequence=VSP_001673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist. Experimental
confirmation may be lacking for some isoforms;
Name=1; Synonyms=GCSFR-1;
IsoId=Q99062-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE: NAME=PROW; NOTE=CD guide CD114 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".
X55721; CAA39253.1;
X55720; CAA39252.1;
S71484; AAB20660.1;
M59818; AAA63176.1;
M59819; AAA63177.1;
M59820; AAA63177.1;
M59820; AAA63178.1;
AY148100; AAN05790.1;
                                                                                                                                                                                                                      an email to license@isb-sib.ch).
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PDB; 1AZ7; 28-JAN-98.
Genew; HGNC:2439; CSF
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hemtopoptn_L_F2.
Pfam; PF00041; fn3; 3.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                   SPTREMBL 23:*
1: sp_archea:*
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3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-892-949-2_COPY_20_227
1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830525 seqs, 258052604 residues
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
sp_plant:*
sp_vodent:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	89	7	δ	ហ	4.	ω	N	<b>-</b>	Result No.
178.5	191	194	198	203	204	209	229	231	231	278	287	502.5	502.5	1121	1121	Score
15.9	17.0	17.3	17.7	18.1	18.2	18.6	20.4	20.6	20.6	24.8	25.6	44.8	44.8	100.0	100.0	Query
626	809	292	861	848	710	861	425	422	422	918	881	716	716	732	509	Query Match Length
13	11	11	φ	σ	13	σ	11	4	4	13	13	11	11	4	4,	DB
Q90WG7	12r66ð	Q8C7G1	Q8MJS1	Q8WN24	057520	Q9BEG2	Q9JM58	075462	Q9UHH5	Q9W6U9	057519	Q8R501	Q8K5B1	Q8NI17	OFAM8D	ID
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	Q99jz1 mus musculu		Q8mjsl sus scrofa	Q8wn24 sus scrofa	O57520 xenopus lae	Q9beg2 bos taurus	Q9jm58 mus musculu	075462 homo sapien	Q9uhh5 homo sapien	Q9w6u9 gallus gall	O57519 xenopus lae	Q8r501 mus musculu		Q8ni17 homo sapien	Q8wyj0 homo sapien	Description

45	44	43	42	41	40	39	38	37	36	3 5	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
140.5	141.5	142	144	145	146.5	146.5	148.5	148.5	149.5	151.5	153	153	153	153	153	153.5	154	154	154.5	156	156	158.5	160	162	165.5	169	172	172.5
12.5	12.6	12.7	12.8	12.9	13.1	13.1			13.3	13.5	13.6	13.6	13.6	13.6	13.6	13.7	13.7	13.7	13.8	13.9	13.9	14.1	14.3	14.5	14.8	15.1	15.3	15.4
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	Q90zi6 paralichthy	Q16542 homo sapien	cani	O46386 mustela vis	P70225 mus musculu	O88507 mus musculu		xen		Q8jft3 brachydanio	οmo	Omo	Omo	Omo	Q16354 homo sapien	w	Q9xs92 trichosurus	O93404 oreochromis	Q9ptp0 carassius a	Q8vhk6 rattus norv	O88786 mus musculu	070535 rattus norv	ュ		Q9pth9 xenopus lae	Q9n0j7 callithrix	c	Q8qg54 cyprinus ca

# ALIGNMENTS

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121 IQIEWIKDELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVI 180	93 SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 152	61 SCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRM 120	33 ALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAPGEKHDNCTTNSSTSENRA 92	1 ALPAKPENISCVYYYKKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRA 60	Query Match 100.0%; Score 1121; DB 4; Length 509; Best Local Similarity 100.0%; Pred. No. 5.5e-98; Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 509 AA; 58390 MW; 5DC85C59E170D44B CRC64;	SMART; SM00060; FN3; 3.	0041; fn3; 2	IPR003961;	InterPro; IPR002996; CR1A.	6452.1;	the EMBL/	ole type I cytokine recep	Zhang W., Wan T., He L., Yuan Z., Cao X.;	SEQUENCE FROM N.A:	[1]		Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	CRL3.	<b>p</b> ,	(TrEMBLrel. 21, Last annotation	(TrEMBLrel. 20,	2002 (TrEMBLrel.	~	Q8WYJO PRELIMINARY; PRT; 509 AA.		

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MEDLINE=21988187; PubMed=11877449;
MEDLINE=21988187; PubMed=11877449;
MEDLINE=21988187; PubMed=11877449;
MEDLINE=21988187; PubMed=11877449;
MEDLINE=2198819 J.A., Yi S., Gurney A., De
"A Novel Type I Cytokine Receptor Is Expressed on Mos
Proliferation, and Activates STAT-3 and STAT-5.";
J. Biol. Chem. 277:16831-16836(2002).

BEBL; AF486620; AAM279581; -.

RINEETPRO; IPR003961; FN_III.

PIAM; PF00041; FN3; 1.
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Best Local :
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01-OCT-2002
01-OCT-2002
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SEQUENCE FROM N.A.
MEDLINE=21988187; PubMed=11877449;
Ghilardi N., Li J., Hongo J.A., Yi
"A Novel Type I Cytokine Receptor:
                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SEQUENCE
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nomura H., Yaguchi N., "Polymorphism between (receptor NR10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine receptor
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SEQUENCE
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InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6;
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                            2 LPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRAS
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; IPR003961; FN_III.
00041; fn3; 1.
M00060; FN3; 3.
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                                                                             CSFFLPRITI--PDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKR
                                      ASYSFPRSCAMPPDICSVEVQAQNGDGKVKSDITYWHLISIAKTEPPIILSVNPI--CNR
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                                                                                                                                                                                                                                                         44.8%; ilarity 49.8%; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                 80598 MW;
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1 C57BL/6
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                                                                                                                                                                                                                                                         Score 502.5;
Pred. No. 4.1e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
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Pred. No. 4.1e-39;
9; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39E6B0B253F7C7E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              CBFB718DCCD40FC7 CRC64;
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nd Balb/c i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the novel cytokine
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                                                                                                                                                                                                                                                            59;
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Best Local :
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01-NOV-1999
01-NOV-1999
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Glycoprotein
GP130.
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01-JUN-1998
01-MAR-2003
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"Partial characterization of putative Xenopus submitted (JAN-1998) to the EMBL/GenBank/DDBJ EMBL; AF041845; AAC03531.1; -. HSSP; P40189; 1BQU. InterPro; IPR00396; CR1A. InterPro; IPR003961; FN III. InterPro; IPR003961; FN III.
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XGP130.
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SMART; SM00060; FN3; 3.

PROSITE; PS01353; HEMATOPO REC_L F2; 1.

SEQUENCE 881 AA; 99003 Mw; 7DE7942D211138A0 CRC64;
                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
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Eukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                057519;
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                                         Archosauria;
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                                                                                                                             ycoprotein
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                                           Aves;
                                    Neognathae;
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No. 1.5e-18;
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ia; Pipoidea; Pipidae;
                                      Vertebrata; Eutei
nes; Phasianidae;
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RESULT 7
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Q9UHH5;
01-MAY-2000
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SEQUENCE
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EMBL; AJ011688; CAB42084.1; -.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                    PROSITE;
                                                                                                                                                             InterPro; IPR007110; Ig
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
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Lok S., Presnell S.R., Jelmh
Foster D.C., Adams R.L., Leh
Submitted (AUG-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class I cytokine receptor.
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                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                 EMBL; AF178684; AAD54385.1; HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hemtopoptn_L_F2.
Pfam; Pr00041; fn3; 4.
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                                                                                                                                                                                                                                 interPro;
                                                                                                                                                                                                                                                       interPro;
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DTASPRTSFSIQGLRPYTEYVFSIRCMKEDGVGFWSDWSEEQIGVTTEDKP
                                                                                                                                       PS50835; IG_LIKE;
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                                                                                                                                                                                                         IPR002996; CR1A.
IPR003961; FN_III.
IPR007110; Ig-like.
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                                                                                              422 AA;
    Conservative
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                                                                                              46315 MW;
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27.7%;
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., Lehner J.M.,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Score 231; DB 4;
Pred. No. 1.2e-13;
4; Mismatches 90
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    90;
                                           Length 422;
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Elson G.C.A., Graber P., Losberger P., Herren S.
Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., G
"CLF-1, a Novel Soluble Protein Shares Homology
Cytokine Type-I Receptor Family.";
J. Immunol. 0:0-0(1998).
                                                                                                                                                                                                                                                                                     Genew; HGNC:2364; CRLF1.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AR059293; ARC28335.1; -. EMBL; AR073515; AAD39681.1; -. HSSP; P16471; 1BP3.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         Magrangeas F., Jacques Y., Minvielle S.; "Cloning and expression of a novel soluble protein containing hematopoietic cytokine receptor domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                075462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 075462
                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                               Receptor;
                                                                                                                                                                                                                                                          SMART; SM00060; FN3; 2.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytokine-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
               114
                                           194
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                                                                                                                         W
                                                                                                                                                   66;
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                                                                                                                                                                 Similarity
              VLGIKRMIQIEWIKPELAPVSSDL----
                                                                                                                PAKPENISCVYYYRKNLTCTWSPGK--ET-SYTQYTVKRTYAFGEKHDNCTTNSSTSENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLGIKRMIQIEWIKPELAPVSSDL----KYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEKPVNISCWSKNMKDLICRWIPGAHGETFLHINYSLKYKLRWYGQDNICEEYHTVGPH-
                                        -SCHIPKDLALFTP-----YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSR
                                                                      ASC---
                                                                                            PEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGLOPFTEYVIALRC-----AVKESKFWSDWSQEKMGMT-EEEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASC-----SFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAKPENISCVYYYRKNLTCTWSPGK--ET-SYTQYTVKRTYAFGEKHDNCTTNSSTSENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AĞLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGGLEDQLSVRWVSP---PALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQ----TSCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SCHIPKDLALFTP--
                                                                                                                                                                                                                                             Signal.
 ::
                                                                                                                                                                                                       38
422 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tactor-1 precursor.
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                                                                  --SFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKP
                                                                                                                                                                                                                     422
                                                                                                                                                                20.6%;
                                                                                                                                                                                                         46301
                                                                                                                                                                                                                                     37
                                                                                                                                                                                                       MW;
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                                                                                                                                                34;
                                                                                                                                                                Score 231; DB 4;
Pred. No. 1.2e-13;
                                                                                                                                                                                                                    CYTOKINE-LIKE FACTOR-1.
                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       AD9DEFCB01B84228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPEVHVSR
                                                                                                                                                   Mismatches
              KYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422
DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                   90;
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, Gauchat J.F.;
gy With Members of the
                                                                                                                                                                             Length 422;
                                                                                                                                                                                                       CRC64;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                  36;
                                                                                                                                                  Gaps
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RESULT 10
Q9BEG9
ID Q9BEG
AC Q9BEG
DT 01-JU
DT 01-JU
DT 01-MA
DE IL-12
GN IL-12
GN IL-12
OS BOS t
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OC Mamma
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RN SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 66; Conserv
                   Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet;
Bovidae; Bovinae; Bos.
NCBI TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9JM58;
01-OCT-2000
01-OCT-2000
                                                                                                            Q9BEG2;
Q9BEG2;
Q1-JUN-2001 (TrEMBLrel 17,
01-JUN-2001 (TrEMBLrel 17,
01-MAR-2003 (TrEMBLrel 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiroyama T., Iwama A., I "cytokine receptor like Submitted (MAR-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation updat
Cytokine receptor like molecule 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00041; fn3; SMART; SM00060; FN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB040038; BAA92777.1;
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JM58
 SEQUENCE FROM N.A.
                                                                           Bos taurus
                                                                                       IL-12R BETA2
                                                                                                   IL-12 receptor beta2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRLF1 OR CRLM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               # P16471; 1BP3.
# MGI:1340030; Crlf1.
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                                                                                                                                                                                                                                                                                    249
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                                                                                                                                                                                                                                                                                                                                     -SCHIPKDLALFTP-----YEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSR
                                                                                                                                                                                                                                                                                                                                                            ASC-----SFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKP
                                                                                                                                                                                                                                                                                                                                                                                      PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPH-
                                                                                                                                                                                                                                AGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP
                                                                                                                                                                                                                                                         TGLOPFTEYVIALRC-----AVKESKFWSDWSQEKMGMT-EEEAP
                                                                                                                                                                                                                                                                                    VGGLEDQLSVRWVSP--
                                                                                                                                                                                                                                                                                                                                                                                                             PAKPENISCVYYYRKNLTCTWSPGK--ET-SYTQYTVKRTYAFGEKHDNCTTNSSTSENR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002996; CRIA.
IPR003961; FN_III.
                                                                           (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      20.4%;
ilarity 29.2%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 P
46662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A., Nakamura Y.,
like molecule 3."
) to the EMBL/Gen
                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                    -PALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 229;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
910535C629CA7056
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 229; DB 11; ed. No. 1.9e-13; Mismatches 90
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                                                   Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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ID 05752
AC 0
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                                                                      Query Match
Best Local S
Matches 47
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Best Local
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01-JUN-1998
01-MAR-2003
                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003529; Hemtopoptn_L_F2
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 4.
                                                                                                                                                                                                                               HSSP; P40189; 1BQU.
InterPro; IPR003961; FN III.
InterPro; IPR003529; Hemtopoptn_L_F2
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                           Chen J., Grace A., Chien K.R.;
"Partial characterization of putative Xenopus
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF041846; AAC03532.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           057520
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Submitted (FEB-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lymph node;
Waldvogel A.S., Za
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNĀL
                                                                                                                                                                                                     PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287
58 NRASCSEFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LPAKPENISCVYY-YRKNLTCTWSPGKETS-YTQYTVKRTYAFGEKHDNCTTNSSTSE--
                                                                        . Similarity 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNF--AKNRKDKNQTYNLTGLQP
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861 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. (TrEMBLrel.
                                                                        Conservative
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                                                                                                                                                                  ĀΑ;
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861 I
96208 MW;
                                                                                           18.2%;
                                                                                                                                                               79849 MW;
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to the EMBL/GenBank/DDBJ databases.
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                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                      Score 204; DB
Pred. No. 8.6e
31; Mismatches
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Last annotation update)
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Pred. No. 3.
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IL-12 RECEPTOR BETA2
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                                                                                                                                                             BFA7C77E32B6CE6F CRC64;
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                                                                                                              DB 13;
                                                                                           .6e-11;
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                                                                      70;
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databases.
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                                                                                                              Length 710;
                                                                      Indels
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RESULT 13
Q8MJS1
ID Q8MJS
AC Q8MJS
DT 01-OC
DT 01-OC
DT 01-MB
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OS Sus s
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Best Local S
Matches 65
           QBMJS1;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
Interleukin-12 receptor b
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Q8WN24;
01-MAR-2002
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NON TER
NON TER
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"Limited effect of recombinant porcine interleukin-12 on lymphocytes due to a low expression of IL-12 Beta2 recept Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF448143; AAL60218.1;
                                                                                   CSLW8D
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.MAR-2002 (TrEMBLrel. 20, 01.MAR-2002 (TrEMBLrel. 20, 101.MAR-2003 (TrEMBLrel. 23, 1101.MAR-2003 (TrEMBLrel. 23, 1101.MAR-2003 (TrEMBLrel. 23, 1101.MAR-2003)
  Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hemtopoptn_L_F2
Pfam; PF00041; fn3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                     2 LPAKPENISCVYY-YRKNLTCTWSPGKETS-YTQYTVKRTYAFGEKHDNCTTNSSTSE--
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                   CDSLDLGINLPPESPESSYTAQVTAINSLGTASSFPCTFTLLDVVRPLPPWDIRIKCVNA
                                                                                                                                                                                                                                                                                                                         VPEQPONVSCMOKGERGTVACSWDRGRDTHLYTAYTLQLN---GPK--NLTWQKQCSDYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVIALRCAVKESK-FWSDWSQEKMGMTEEEAP 208
                                                                                                                                                        EYEFQISSKPHLQKGRWSDWSESLRTQTPEKEP
                                                                                                                                                                                                              SMSTCTLQWRDEGLV-----LLNRLRYRPVYSRSWNMVN-ATNAKGR--
                                                                                                                                                                                                                                       IKRMIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFT
                                                                                                                                                                                                                                                                                               -NRASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIFRVKPVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNALKIKWRNPLLNAFT--LKYNIRYRPVKNQDW-EMVPEEDTASHRDSFTLQDLLPYTE
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                                                                                                                                                                                 EYVIALRCAVKESK-FWSDWSQEKMGMTEBEAP
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848
848 AA;
(Pig).
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                     PRELIMINARY;
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94753 MW; AD66C885A27DA427 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                18.1%; Score 203; DB 6; 30.5%; Pred. No. 1.3e-10;
                22, (
22, 1
23, 1
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              Last sequence update)
Last annotation update)
a 2.
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Last annotation update)
a 2 chain (Fragment).
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ά C.,
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., Valencia
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Sus.
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RESULT
Q8C7G1
                                                                                                                                                                                                                         Query Match
Best Local
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Best Local
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"Cloning of ;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Liver;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II '
"Analysis of the mouse transcriptome based on functional of the mouse tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8C7G1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel 23, Created)
01-MAR-2003 (TrEMBLrel 23, Last sequence update)
01-MAR-2003 (TrEMBLrel 23, Last annotation update)
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InterPro; IPR003961; FN III.
InterPro; IPR003299; Hemtopoptn_L_F2.
InterPro; IPR00329; Hemtopoptn_L_F2.
SMART; SM00060; FN3; 4.
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[1]
                                                                                                                                                                                                                                                                                                        SEQUENCE
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI
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                                                                                                                                    PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
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                                                                                    PGKPE1HKCRSPDKETFTCWWNPGSDGGLPTNYSL--TYSKEGEKNTYECPDYKTSGPN-
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                                                                                                                                                                                                                                                                                                      292 AA;
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                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                      33618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96055 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.7%;
                                                                                                                                                                                                                      17.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                       Score 194; DB 11;
Pred. No. 2.5e-10;
7; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 198; DB 6; Length 861; Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2AB663E3C5F42534 CRC64;
                                                                                                                                                                                                                                                                                                      9D60422B59E88A19 CRC64;
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                                                                                                                                                                                             92;
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                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                292;
                                                                                                                                                                                                                                                                                                                                                                                                                    annotation
                                                                                                                                                                                             18;
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RESULT 15
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Search completed: August
Job time : 76.6152 secs
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2001) to the EN
EMBL; BC005555; AAH05555.1; -
EMBL; BC006652; AAH06652.1; -
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99JZ1
Q99JZ1;
01-JUN-2001 (TrembLrel. 1
01-JUN-2001 (TrembLrel. 1
01-QCT-2002 (TrembLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopo;
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:97763; Prlr.
                                                                                                           194
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                                                                                                           GQKYLVQTRCK-PDHGYWSRWGQEK
                                                                                                                                                           FTEYVIALRCAVKESKFWSDWSQEK 199
                                                                                                                                                                                                                                                              KRMIQIEWIKPELAPVSS----DLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQP
                                                                                                                                                                                                                                                                                                                                                                       ASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPK--IFRVKPVLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKPEIHKCRSPDKETFTCWWNPGSDGGLPTNYSL--TYSKEGEKNTYECPDYKTSGPN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAKPENISCVYYYRKNLTCTWSPGKETSY-TQYTVKRTYA-FGEKHD-NCTTNSSTSENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQKYLVQTRCK-PDHGYWSRWGQEK
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                                                                                                                                                                                                               KTYLWVKWLPPTITDVKTGWFTMEYEIRLKSEEADEW-EIHFTGHQTQ----FKVFDLYP
                                                                                                                                                                                                                                                                                                                        -SCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTLEVKQLKDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68223 MW;
                           18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 191; DE 27.8%; Pred. No. 1.26 tive 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hemtopoptn_L_F1
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17,
22,
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, Last sequence upo
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                              13:30:16
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L.2e-09;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1017
1017
1017
1017
1017
1010
514.5
514.5
514.5
                                                                                                                                                                                                                           Score
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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Gapop 10.0 ,
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    100.00
100.00
50.30
50.66
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1017
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
                                                                                                                                                                                                                           Length
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ABB05730
ABP54364
ABP54365
AAE24024
ABB05738
AAB51244
AAE24029
      ABB05741
                                                                                                                                                                                                                                                                                               SUMMARIES
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Novel human diagno Human zcytor17 pro Human xcytor17 pro Human NR10.4 splic Human NR10.4 splic Human haematopoiet Human zcytor17 pro Human haemopoietin Human HPRI variant Human zcytor17 pro
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### ALIGNMENTS

RESULT 1 ABG05070 ID ABG0

ABG05070 standard; Protein;

620 AA

Novel human diagnostic protein #5061.

forensic

13-FEB-2002 (first entry)

ABG05070;

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WPI; 2001-639362/73.
N-PSDB; AAS69257.
                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
New isolated polynucleotide and encoded polypeptides, useful in
                                           Drmanac RT,
                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                          11-OCT-2001.
                                                                                                                                          WO200175067-A2
                                                                                                                                                            Homo sapiens.
                                                            (HYSE-) HYSEQ INC.
                                          Liu C,
                                          Tang
                                            YŢ,
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RESULT 2
ABBO5730
ID 85730
AB 850730
AC ABBO
XX ABBO
XX ABBO
XX O1-M
XX O1-M
XX O2-V
KW ANTI
CX W ANTI
C
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Note: The sequence data for this patent did not appear in the printed are ferring the product of the printed of the invention.
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Best Local (
      03-JAN-2002
                                                                                                                                                                                         Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiviral; antirheumatic; antiarthritic; cytostatic; muscular; lymphoid; immune; inflametory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                    WO200200721-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zcytor17
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                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB05730
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Pred. No. 1.2e-93;
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RESULT 3
ABP54364
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AC ABP5
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DE Huma
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KW NR10
KW NR10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease;
                                                Human NR10.4 splicing variant protein SEQ ID NO:4.
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                                                                                     20-JAN-2003
                                                                                                                       ABP54364;
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Maurer MF;
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29-JUN-2000;
                                                                                                                                                       ABP54364 standard; Protein; 764 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention.
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ilarity 100.0%;
Conservative (
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; 2000US-214955P.
; 2001US-267963P.
                                                                                   (first entry)
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Matches 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietic receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.4
                                                                                                                          ABP54365
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                                                                          Human NR10.4
                                                                                                   20-JAN-2003
                                                                                                                                                ABP54365 standard;
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                                 NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing variants of hematopoietin receptor proteins and s, applicable in searching hematopoietic factors and develdies for immunological and hematopoietic diseases.
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                                                                                                                                                                                                                                      LPEHTKGEV 189
                                                                                                                                                                                                                                                                          PRKSQYLRSRMPEGTRPEAKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLVSEK
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                         disease; haematopoietic cell
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Pred. No. 1.6e-93;
                                                                         protein SEQ ID
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Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes haematopoietic receptor NR10 splicing variants (1). (1) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.4
osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
                                                                                      cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
                                                                                                                                                 Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation; pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; osteoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                        Human haematopoietin receptor 1 (HPR1) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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Pred. No. 1.6e-93;
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Misc-difference
                11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
                                WO200229060-A2
                                                                                                   Domain
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33..24
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                                                                                                                                                                                                      563..573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                 note= "WSXWS motif"
                                                                                                                                                                                                                                                                                                                                                                                                  note= "This residue changes
llelic variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "This residue changes
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "C-terminal cytokine receptor subdomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "This residue changes to Ala during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Cytokine receptor domain"
                                                        note= "This residue changes to Gly during
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llelic variation"
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                                                                                                                                         "Repeat peptide'
                                                                                                                                                                            "Repeat
                                                                                                                                                                                            "Box1 conserved motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Proline-rich linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human mature HPR1 protein"
                                                                                         "Box2 conserved motif"
                                                                                                        "Repeat peptide"
                                                                                                                                                                                                                             "Core transmembrane domain"
                                                                       "Repeat peptide"
                                                                                                                         "Repeat peptide'
                                                                                                                                                                                                            "Cytoplasmic domain"
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05-OCT-2001; 2001WO-US31634

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LPEHTKGEV

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557 · KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL

VIDKLYVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI 120

VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI

676

616 60

PPRKSQYLRSRMPEGTRPEAKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLVSEK 180

PPGKSQYLRSRMPEGTRPEAKEQLLFSGQSLVPDHI

736

1 KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL

121

Matches Query Match

188;

Conservative

0

Mismatches

Local Similarity

99.3%;

Score 1010; DB 23 Pred. No. 7.8e-93;

DB 23;

Length 745; Indels

0;

Gaps

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CC treating cell proliferation conditions such as leukaemia and tumour cells. HPR sequences are also useful for treating gell proliferation conditions and excess of bone-resorbing CC cells. HPR sequences are also useful for treating medical conditions and Cd diseases such as cell proliferation, metabolic and reproductive hormone CC ellated conditions. They are useful for treating various haematologic and concologic disorders e.g., Epstein-Barr virus-positive masopharyngeal CC carcinoma, myslogenous leukaemia, colon, stomach, prostate, renal cell, CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia CC of chronic disease, aplastic anaemia, Fanconi's saplastic anaemia), myelo-CC dysplastic syndromes (including refractory anaemia, refractory anaemia (c.g., anaemia CC paenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/CC myeloid metaplasia, osteoclast disorders that lead to bone loss such CC as osteoporosis including post-menopausal osteoporosis, periodontitis (c.g., anaemia including creutsfeld-Jacob disease, demyelianin-Barra syndrome, vertebral disc disease, demyelianin gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPRL and HPR2 polypeptides are also useful cerebral ischaemic diseases. HPRL and HPR2 polypeptides are also useful constitutions of the constitution o
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating cell proliferation conditions e.g., pancytopaenia, leukoj anaemia, thrombocytopaenia, neurodegenerative disorders and osteoj resulting from a lack of bone-forming cells. They are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 84-87; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000; 2000US-238706P
13-OCT-2000; 2000US-240476P
20-FEB-2001; 2001US-270282P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human and murine haematopoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human and murine hematopoietin receptor polypeptides HPR1 and HPR2, useful for treating cell proliferation, metabolic, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cosman
                                                                                   deficient mammary development and infertility. The
                                                                                                              cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides HPR1 and HPR2. Sequences of the invention are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating cell page related conditions
                                                     HPR1
745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mosley BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation conditions e.g., pancytopaenia, leukopaenia, mbocytopaenia, neurodegenerative disorders and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΤA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dubose RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiley
                                                                                   present sequence
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RESULT 6
ABB05738
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                                                         맑
                                                                                                                                                                                                                            2 Cytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, cantirheumatic, antiarthritic and muscular activities. The zcytor17 cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 cytor17 cytor17 cytor17 cytor17 cytor17 antibodies are useful for treating lymphoid, immune, immune, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent seguences used in the cemplification of the present invention.
                                                                                                                              Query Match
Best Local S
Matches 97
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 195-197; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscular; tymphonon, infection; multiple sclerosis; cancer; infection; immunosuppression; cytotoxicity; multiple sclerosis; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; autoimmune disease; vancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABA93803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2000; 2000US-214282P.
29-JUN-2000; 2000US-214955P.
08-FEB-2001; 2001US-267963P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200200721-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antiviral; antirheumatic; antiarthritic;
muscular; lymphoid; immune; inflammatory; spleenic; blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB05738 standard; Protein; 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spleenic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001; 2001WO-US20484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a cytokine receptor designated zcytor17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                         544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-090519/12.
                      61
                                                                                                                            97;
                                                                                          Н
                                                                                                                                              Similarity
VIDKLYVNFGNVLQEIFTDEARTGQENNLGGEKNG---YVTCP 100
                                                     KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
                                                                          KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blood or bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 5; 5q11; cytokine receptor; immunomodulatory;
mmatory; antiviral; antirheumatic; antiarthritic; cytosta
                                                                                                                                                                                                  649
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Presnell SR,
                                                                                                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                              50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gao
                                                                                                                            ۲,
                                                                                                                            Score 514.5; DB 1
Pred. No. 6.1e-43;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxicity; leukopenia; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitmore TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO:46
                                                                                                                                                             DB 23;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuijper JL;
                                                                                                                                                           Length
                                                                                                                                                               649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
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RESULT 8
AAE24029
ID AAE2
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AC AAE2
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies and haematopoietic disorders including autoimmune diseases and allergies
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of immune and diseases and allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-061720/07.
N-PSDB; AAC92350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmembrane; immune disorder; haematopoietic disorder; autoimmune disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 13-14; 127pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hematopoietin receptor protein NR10 for screening potential ligands for treatment of immune and hematopoietic disorders such as autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2000; 2000WO-JP03556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human haemopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB51244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB51244 standard; Protein; 662 AA.
                                            AAE24029 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200075314-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                  as metal
                                                                                                                                                                                557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy; pollen allergy.
                                                                                                                                                  61
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                           VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNG---YVTCP 100
                                                                                                                                                                                               KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGTRILSSCP 646
                                                                                                                    VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGTRILSSCP
                                                                                                                                                                                                                                                                                                    662 AA;
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                  and pollen allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0155797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0217797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor protein NR10.3 SEQ ID NO:17
                                            Protein; 662
                                                                                                                                                                                                                                                      50.6%;
                                                                                                                                                                                                                                       Score 514.5; DB 22;
Pred. No. 6.2e-43;
"Widmatches 2;
                                            Ä
                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                              and allergies
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<del>-</del>-
                                                                                                                                                                                                                                          Gaps
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AAE24029;

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cancer; myclodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation, pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; osteoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischaemic disease; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematologic
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05-OCT-2001; 2001WO-US31634.

06-OCT-2000; 2000US-238706P. 13-OCT-2000; 2000US-240476P. 20-FEB-2001; 2001US-270282P.

(IMMV ) IMMUNEX CORP.

BA, Bird ŦĂ, Dubose RF, SR

Human and murine hematopoietin receptor useful for treating cell proliferation, hormone related conditions polypeptides HPR1 and HPR2, metabolic, and reproductive

Disclosure; Page 112-115; 136pp; English

CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including CC carcer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, carcinoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-dyplastic syndromes (including refractory anaemia, refractory anaemia curvità ringed sideroblaste or with excess blasts), idiopathic thrombocyto-dyplastic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/ curvità myelodimetaplasia, osteoclast disorders that lead to bone loss such cas osteoporosis including post-menopausal osteoporosis, periodontitis cresulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, curvitations (e.g., acute polyneuropathy, The present invention relates to human and murine haematopoietin receptor polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, mammary development and infertility.

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RESULT 9
ABB05741
ADB057941
ADB05794
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The present invention describes a cytokine receptor designated zcytor17. CC Zcytor17 has immunomodulatory, antiinflammatory, antivital, cytostatic, CC antirheumatic, antiarthritic and muscular activities. The zcytor17 CC antirheumatic, antiarthritic and muscular activities. The zcytor17 CC proteins are useful for treating and diagnosing lymphoid, immune, CC anti-zcytor17 antibodies are useful in stimulating lymphoid as in the immunity and for stimulating lymphocyte proliferation, such as in the CC treatment of infections involving immunosuppression, including certain cyiral infections. They are also useful for inducting cytotoxicity and CC viral infections. They are also useful for inducting cytotoxicity and CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple colerosis), inflammatory diseases (e.g. Crohn's disease), cancer, CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to CC chromosoma 5, specifically to the 5q11 chromosomal region. ABA93767 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2000;
29-JUN-2000;
08-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiinflammatory; antiiviral; antiirbeumatic; antiarthritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 204-206; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spleenic, blood or bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotide useful for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABA93808.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-090519/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2000US-214282P.
; 2000US-214955P.
; 2001US-267963P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding a cytokine receptor diagnosing lymphoid, immune, disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 514.5;
Pred. No. 6.
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RESULT 10
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Pred. No. 6.2e
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                                                                                                 Score 514.5; DB 24; Pred. No. 6.5e-43; 1; Mismatches 2;
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No. 6.2e-43;
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RESULT 11
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DB; ABQ83373.
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                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                0,
                                                                                                                                                                                                                Gaps
                                                                                                        60
                                                                                                                                                                155
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RESULT 12
ABP54370
ID ABP54
XX
AC ABP54

ABP54370

standard;

Protein;

716

A

ABP54370;

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RESULT 13
AAE24037
ID AAE24
XX
AC AAE24
XX
AC AAE24
XX
AC AAE24
XX
XX
XX
DT 23-SE
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietic receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the mouse mNR10Balb-to the receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic cell regulation.
               23-SEP-2002
                                         AAE24037;
                                                                AAE24037 standard;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 30-32; 250pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABQ83370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2001; 2001JP-0087298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2002; 2002WO-JP02769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277230-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-018925/01.
                                                                                                                                                                                                                                          588
                                                                                                                                 706
                                                                                                                                                           179
                                                                                                                                                                                     648
                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                            531
                                                                                                                                                                                                                                                                                                                                               107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mNR10Balb-c
                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                        KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
                                                                                                                                                                                                      PPRKSQYLRSRMPEGTRPEAKEQLLFSGQS--LVPDHLCEEGAPNPYLKNSVTAREFLVS
                                                                                                                                                                                                                                        LIDKLVVNFENFLEVVLTEEAGKGQASILGGEANEYVTSPSRPDGPPGKSFKEPSILTEV
                                                                                                                                                                                                                                                                                            RKPNRLTPLCCPDVPNPAESSLATWLGDGFK-KSNMKETGNSGNTEDVVLKPCPVPAD--
                                                                                                                                  ENI PEHSKGEV
                                                                                                                                                           EKLPEHTKGEV 189
                                                                                                                                                                                     ASEDSHSTCSRMADEAYSELARQPSSSCQSPGLSPPR--EDQAQNPYLKNSVTTREFLVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                    716 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                Conservative
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing
                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                            47.5%;
                                                                                                                                  716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hasegawa
                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variant
                                                                  726
                                                                                                                                                                                                                                                                                                                                          Score 483.5; DB 2*;
Pred. No. 9.2e-40;
"" amatches 57;
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                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H
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                                                                                                                                                                                                                178
                                                                                                                                                                                     705
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                                                                                                                                                                                                                                                                                            587
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Mouse haematopoietin receptor 1 (HPR1) protein.
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Mouse; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation; pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; osteoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; ischaemic disease; myasthenia gravis; chronic neuronal degeneration; ischaemic disease.

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Mus musculus.
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06-OCT-2000; 2000US-238706P.
13-OCT-2000; 2000US-240476P.
20-FEB-2001; 2001US-270282P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Human and murine hematopoietin receptor useful for treating cell proliferation,
                                       WPI; 2002-330172/36.
N-PSDB; AAD38776.
                                                                                                                                                                                        05-OCT-2001; 2001WO-US31634
                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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                                                                              Cosman DJ,
                                                                                                                                                                                                                                           WO200229060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                              Mosley BA,
                                                                                                                                                                                                                                                                                  /note= "B
612..622
                                                                                                                                                                                                                                                                                                                                                                                           /note=
517
                                                                                                                                                                                                                                                                                                             /note= "Encoded 547..557
                                                                                                                                                                                                                                                                                                                                       718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            note= "Encoded by ATT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                    note= "Encoded"
                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "N-terminal cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Mouse mature HPR1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 533
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Core transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cytokine receptor domain"
                                                                                                                                                                                                                                                                                                "Box1
                                                                                                                                                                                                                                                                                                                                                                                                       "WSXWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Extended transmembrane domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Proline-rich linker"
                                                                                                                                                                                                                                                                      "Box2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "C-terminal cytokine
                                                                               Bird
                                                                                                                                                                                                                                                                                               conserved motif"
                                                                               TA,
                                                                                                                                                                                                                                                                    conserved
                                                                                                                                                                                                                                                                                                                                                                                                       motif"
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                                                                                                                                                                                                                                                                                                                                                    GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat"
                                                                                                                                                                                                                                                                      motif"
 polypeptides HPR1 and HPR2, metabolic, and reproductive
                                                                                RF,
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                                                                               Wiley
  and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdomain"
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hormone Claim 2

related

conditions

2; Page 105-108; 136pp; English

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RESULT 14
ABP54371
ID ABP54
XX ABP54
XX ABP54
XX ABP54
XX ABP54
XX ABP54
XX NGUS6
XX NGUS6
XX NR10;
XW haema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             squamous cell carcinoma), haematologic disorders anaemias (e.g., anaemia of chronic disease, aplastic anaemia, refractory anaemia, refractory anaemia with ringed sideroblasts or with excess blasts) idiopathic thrombocytopaenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/ myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, periodontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeld-Jacob disease, demyelinating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including fatigues including fatigues of the conditions (e.g., acute polyneuropathy, cuillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancer-associated cachaxia, fatigue, solid tumours (e.g., osteosarcoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human and murine haematopoietin receptor polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis
                                                                Mus musculus
                                                                                                                              haematopoietic
                                                                                                                                                             NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease;
                                                                                                                                                                                                                                                     Mouse mNR10c57BL-6 splicing variant protein SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                             20-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP54371 standard; Protein; 716 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sarcoma), carcinoma (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting from a lack of bone-forming cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 LIDKLVVNFENFLEVVLTEEAGKGQASILGGEANEYVTSPSRPDGPPGKSFKEPSILTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VIDKLYVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KKPNKLTHLCWPTVPNPABSSIATWHGDDFKDKLNLKESDDSVNTEDRIILKPCSTPSDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPR1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                          disease; haematopoietic cell regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , fatigue, solid tumours (e.g., osteosarcoma, adenocarcinoma (for example, breast cancer),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 483.5; DB 2
Pred. No. 9.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                         immunological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726;
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AAB51242

AAB51242

XX

AC AABE

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Matches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietic receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the mouse mNR10c57BL-6 profess from the present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                              immunoregulation; haematopoietic cell reguimmune disorder; haematopoietic disorder;
metal allergy; pollen allergy.
                                                                                                                                                                                                                                                                                                                                Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB51242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB51242 standard; Protein;
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                                                                 WO200075314-A1
                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                        Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
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DB; ABQ83371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 LIDKLVVNFENFLEVVLTEEAGKGQASILGGEANEYVTSPSRPDGPPGKSFKEPSVLTEV
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                                                                                                                                                                                                             haematopoietic cell regulation; transmembrane; naematopoietic disorder; autoimmune disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                            entry)
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Pred. No. 2.3
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Search completed: August 18, Job time: 72.829 secs
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                                                                                                                                                                       Query Match 45.4%; Sc Best Local Similarity 100.0%; P Matches 86; Conservative 0;
                                                                                                                                                                                                                                                             The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and pollen allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hematopoietin receptor protein NR10 for screening potential ligands for treatment of immune and hematopoietic disorders such as autoimmune diseases and allergies -
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-061720/07.
N-PSDB; AAC92337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 3-5; 127pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maeda M,
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                                                        61 VIDKLVVNFGNVLQEIFTDEARTGQE 86
                                                                                                                    557
                                                                                                                 Yaguchi N;
                                                                                                                                                                                                                                      652 AA;
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99JP-0217797.
             2003, 13:27:01
                                                                                                                                                                          Score 462; DB 22;
Pred. No. 1.2e-37;
0; Mismatches 0;
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No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 0.5
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1017
1 KKPNKLTHLCWPTVPNPAES......VTAREFLVSEKLPEHTKGEV
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     Copyright
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
     GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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US-08-889-841B-10
US-08-938-291A-6
US-08-938-291A-6
US-08-938-291A-6
US-09-589-619-6
US-09-206-551-13
US-09-206-551-11
US-09-206-551-11
US-09-206-551-11
US-09-206-551-12
US-09-419-252-991A-26008
US-09-472-240A-5
US-08-489-841B-28
US-09-419-362-35
US-09-419-362-36
US-08-889-841B-36
US-08-889-841B-36
US-08-889-841B-36
US-08-889-841B-36
US-09-419-362-36
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US-09-419-362-39
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                      Sequence
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                  10, Appl
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11, Appl
12, Appl
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13, Appl
14, Appl
14, Appl
26, Appl
27, Appl
28, Appl
29, Appl
20, Appl
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RESULT 2 US-09-419-362. ; Sequence 10; ; Datent No.; ; GENERAL INFE; ; APPLICANT; ; TITLE OF II; ; FILE REFERE; ; CURRENT AP; ; CURRENT FII;	0 Q Q D .	Query Matc Best Local Matches Qy Db 3	RESULT 1 US-08-889-8411 Sequence 10 GENERAL INFO APPLICANT: TITLE OF 11 FILE REFERI CURRENT APPLICARENT FILE PRIOR APPLI PRIOR APPLI PRIOR FILE I PRIOR FILE I PRIOR TILE I PR		222 222 222 222 232 242 242 263 263 263 263 263 263 263 263 263 26
10, 10, 0. 65 INFOR NT: B F INV FEREN APPL		5 0 7 4 S	9-841B-10 UCC 10, Application U L INFORMATION: CANT: BETMAN, Philli OF INVENTION: HIV E REFERENCE: 14918-703 NT APPLICATION NUMBER: FILING DATE: 1996-84 APPLICATION NUMBER: FILING DATE: 1996-9 R OF SEQ ID NOS: 57 ARE: FASTSEQ for Win NO 10 TH 491 HIV 9-841B-10		81 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8.
ion hill hill HIV 8-70 NUME		9.0% imilarity 23.0% ; Conservative ; Conservative ; HILCWPTVPNPAESSI- ; HI	S/O D W NVB R: 7-O US 7-O		555161 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
US/09419362 LID W. ENVELOPE POLYPEPTIDES J3DIV1 BER: US/09/419,362		imilarity 23.0%; Score 92; DB 3; Length 491; conservative 23; Mismatches 69; Indels 72; Gaps; Conservative 23; Mismatches 69; Indels 72; Gaps; Conservative 23; Mismatches 69; Indels 72; Gaps; Conservative 11; CWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK	8889841B LOPE POLYPEPTIDE US/08/889,841B 7-08 60/676,737 8	ALIGNMENTS	US-08-037-8 US-08-530-1 US-08-530-1 US-08-689-1 US-08-99-796-2 US-08-037-8 US-08-530-1
AND	ERGERKNCSFNITT EELLPVSPEIP   : :     EPIPIHYCAPAGFA DHLCEE 159       LAEE 230	DB 3; Len 0.12; ches 69; LNIKESDDSVNT: : :   :: NVBQMHEDIISL	S AND	TS	-816A-20 -816A-24 -146-29 -841B-25 -841B-25 -362-25 -362-26 -816A-16 -816A-28 -146-16 -146-22 -146-22 -146-22 -146-23 -816A-18 -816A-18 -816A-18 -816A-18
VACCINE	TTSLRDKGKKEYALFYKLDV PRKSQ 	Length 491; ; Indels 72; ; VNTEDRILKPCSTPS ::                 ISLWDQSLKPCV	VACCINE		Sequenc Seq Sequenc Sequenc Sequenc Sequenc Sequenc Se
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	14 12 20	K 64 8;			Appl Appl Appl Appl Appl Appl Appl Appl

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RESULT 3
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; ORGANISM: HIV
US-09-419-362-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6117673
GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 491
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                   APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
TITLE OF INVENTION: PRODUCTS AND METHODS
                                                                                                                                                                                                                               SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                             APPLICATION NUMBER: US/08/938,291A FILING DATE: September 26, 1997
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204
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                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                             633 West Fifth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plowman, Gregory D.
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                                                                                                                                                                                                                                                                    IBM P.C. DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Street
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Pred. No. 0.12
23; Mismatches
                                                                                                                                                                                                                                                                    5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application Patent No. 6576442 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.0%;
Best Local Similarity 19.3%;
Matches 47; Conservative 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/938,291
FILING DATE: September 26, 1997
APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                    SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plowman, Gregory D.
Schlessinger, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lev, Sima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 TRPEAKEQLLFSGQ------SLVPDHLCEEGAPNPYLKNSVTAREFLVSEKLPEHT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 HVLLLVLHGGTILDTGAGDPSSKKGDANTIANVFDTVMRVHYPSALGRLAIRLVPCP--P
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                                                                                                                                                                           APPLICATION NUMBER: US/09/589,619
FILING DATE: 07-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09589619
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRODUCTS AND METHODS
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Pred. No. 0.
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Best Local (
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/956,483
APPLICATION UNMBER: US 07/956,483
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 017753-055
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                     SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                          FILING DATE: 07-JUN-1995
                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1349 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 TRPEAKEQLLFSGQ------SLVPDHLCEEGAPNPYLKNSVTAREFLVSEKLPEHT 185
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/: United States
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                                                                                                                                                                                                                                                                                                                                                                                                      E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIENY, Marie-Paule
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: gp160 VARIANT
S: 29
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Pred. No. 0.51;
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                                                                                                                                                                                                                                                                                                            US-09-206-551-13
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SEQ ID NO 13
LENGTH: 853
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/206,551B CURRENT FILING DATE: 1998-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Complete Genome Sequences of a TITLE OF INVENTION: Immunodeficiency Virus from a RITLE OF INVENTION: Mangabey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marx, Preston APPLICANT: Shaw, George M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: D6286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Smith, Stephen M.
APPLICANT: Georges-Courbot, Marie Claude
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Amino acid sequence of homologous OTHER INFORMATION: D_ELI lentiviral env protein
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 IVPIDNDSSTNSTNYRLINCNTSAITQACP-KVSFEPIPIH-YCAPAGFAILKCRDKKFN 235
178 IVPIDNDSSTNSTNYRLINCNTSAITQACP-KVSFEPIPIH-YCAPAGFAILKCRDKKFN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 GTGPCTNVSTVQCTHGIRPVVSTQLLLNGS-----LAEE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LCVTLN-----CSDELRNNGTMGNNVTTEEKGMKNCSFNVTTVLKDKKQQVYALFYRLD
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                                                                                                                                                                                        7 THICWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THACVPTDPNPQEIALENVTENFNMWKNNMVEQMHEDIISLWDQSLKPC-----VKLTP 123
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                                                                                                                                                      THACVPTDPNPQEIALENVTENFNMWKNNMVEQMHEDIISLWDQSLKPC-----VKLTP 123
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.9%; Score 90.5; DB 3;
22.3%; Pred. No. 0.18;
tive 21; Mismatches 63;
                                                                                                                                                                                                                                                8.9%; Score 90.5;
22.3%; Pred. No. 0.
                                                                          -CSDELRNNGTMGNNVTTEEKGMKNCSFNVTTVLKDKKQQVYALFYRLD
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                                                                                                                                                                                                                                Mismatches
                                    -CPLGKSFEELPVSPEIPPRKSQYLRSR-----
                                                                                                                                                                                                                                                0.39;
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US-07-956-483-12
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Best Local Similarity
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TITLE OF INVENTION: NOVEL BACKLET
TITLE OF INVENTION: 9p160 VARIANT
OF GROHENCES: 26
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APPLICATION NUMBER: FR 91
FILING DATE: 02-May 1770RNPW 77
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 12-NOV
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236 GTGPCTNVSTVQCTHGIRPVVSTQLLLNGS-----LAEE 269
                                                                                                                                                         65 LVVNFGNVLQEIFTDEARTG--QENNLGGEKNGYVTCPF-----RPD 104
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P.O. Box 1404
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ilarity 22.3%;
Conservative 2
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Pred. No. 0.4;
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; ORGANISM: HIV
US-09-419-362-8
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US-08-889-841B-8
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GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES
FILE REFERENCE: 14918-703CIP
                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09419362 Patent No. 6585979
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Best Local Similarity
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CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/419,362
CURRENT FILING DATE: 1999-10-15
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/889,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 14918-703DIV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES
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                                                                                                                                                                                                                                                                                          LENGTH:
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86 VTLNCTNLENANNTENÄNNTNNYTLGMERGEIKNCSFNITTSLRDKVKKEYALFYKLDVV 145
                                65 LVVNFGNVLQEIFTDEARTGOENNLGGEKNGYVTCPFR------ 102
                                                                          30 THACVPTDPNPQEVVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCV----KLTPLC 85
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                                                                                                                 7 THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK 64
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47; Conservative
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                                                                                                                                                       Conservative
                                                                                                                                                                       8.8%; Score 90; I
22.2%; Pred. No. 0
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Pred. No.
                                                                                                                                                       Mismatches
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                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 12,
Patent No. 6
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Best Local
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LENGTH: 855
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                                                                     APPLICANT: Marx, Preston A. APPLICANT: Shaw, George M. APPLICANT: Smith, Stephen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/206,551B
CURRENT FILING DATE: 1998-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Complete Genome Sequenc TITLE OF INVENTION: Immunodeficiency Virus TITLE OF INVENTION: Mangabey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Smith, Stephen M.
APPLICANT: Georges-Courbot, Marie Claude
APPLICANT: Lu, Chang Yong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hahn, Bear APPLICANT: Gao, Feng
                                                                                                                           APPLICANT: Hahn, Beatrice H. APPLICANT: Gao, Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: D6286
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                        TITLE
                                         APPLICANT:
                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Amino acid sequence of homologous OTHER INFORMATION: A_U455 lentiviral env protein
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                      OF.
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I: Georges-Courbot, Marie Claude
I: Lu, Chang Yong
INVENTION: Complete Genome Sequences of a Simian
INVENTION: Immunodeficiency Virus from a Red-Capped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPC--STP-SDKLV
                                                                                                                                                                                 2, Application US/09206551B 6521739
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                                                                                                                                                                                                                                                                                                                              --GTRPEAKEQLLFSG 148
                                                                                                                                                                                                                                                                                                                                                                 SYRLINCNTSTITQACP-KVSFEPIPIH-YCAPAGFAILKCKDPEFNGKGPCRNVSTVQC
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Pred. No. 1.1;
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RESULT 13
US-07-956-483-14
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CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 12
LENGTH: 855
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 26008
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
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                                                                                                                                                                                                                                                                                                     LENGTH: 423
TYPE: PRT
                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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                                                                                              71 NVLQEIFTDEARTGQENNLGGEKN-GYVTCFFRP 103
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                                                                                                                              PTFPESVADGTVATWH-----
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                                                                  -VLAEIIKNEGDTVLSNELLGKLNEGGAAAPAAP
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UMBER: US 60/094,190
1998-07-27
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 0.44;
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Pred. No. 1.
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US-07-956-483-14
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                               Sequence 5, Application US/08472240A Patent No. 6284248
                                                                                                                                GENERAL INFORMATION:

APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBE
TITLE OF INVENTION: 9p160 VAR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO 92/19742
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KIENY, M
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01
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CITY: Alexandria
STATE: Virginia
                               CITY: Alexandria
STATE: Virginia
                                                                 STREET:
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                 COUNTRY:
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22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                      THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK 64
            Virginia
: United States
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: United States
                                                                 E: BURNS, DOANE, SWECKER & MATHIS
P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B: Burns, Doane, Swecker & Mathis
P.O. Box 1404
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: gp160 VARIANT
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: NOVEL HYB
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29.6%;
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Pred. No. 1.2;
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                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08889841B GENERAL INFORMATION:
                                                Matches
                                                              Query Match
Best Local
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Best Local
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                       NAME/KEY: VARIANT
LOCATION: (1)...(495)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                              FEATURE:
                                                                                                                                                                                             ORGANISM: HIV
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                             ENGTH: 495
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APPLICATION NUMBER: US 0
FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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STRANDEDNESS: not
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Similarity
                                                               Similarity
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28.3%; Pred. No. 1
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                                                          Score 84.5; DB Pred. No. 0.82;
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                                                Mismatches
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Search completed: August 18, 2003, 13:32:21 Job time : 24.3444 secs	199 FAILKCKDKKFNGTGPCSKVSTVQCTHGIRPVVSTQLLLNGSLABE 244	PRKSQYLRSRMPEGTRPEAKEQLLFSGQSLVPDHLCEE 159	140 HMKDKVQKEYALFYKLDIVPIDDNNTSYRLISCNTSVITQACPM-VTFEPIPIHYCAPAG 198		90 NCSDVNNSTNPNDTNTNSTNTTSSTPTATTSSEEKMEKGEIKNCSFNITT 139	54STPSDKLVIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFR 102	31 THACVPTDPNPQEIELVN-VTEDFNMWKNKMVDQMHEDIISLWDESLKPCVKLTPLCVTL 89

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No.
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Listing first 45 s
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Maximum DB
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Perfect score:
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seq length: 2000000000
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   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep: *
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/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep: *
/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep: *
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/ cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep: *
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/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep: *
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US-09-972-708-12
US-09-972-708-14
US-09-972-708-14
US-09-972-708-12
US-09-972-708-12
US-09-972-708-14
US-10-190-435-5
US-10-190-435-128
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           Sequence 2, Appli
Sequence 4, Appli
Sequence 15, Appl
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Sequence 17, Appl
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Sequence 12, Appl
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	8.0	8.0	8.0	8.0		8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1		8.2	8.2			8.2						8.5	8.5
	625	502	502	100	1080	720	720	556	506	506	870	869	862	849	790	790	579	511	1186	1186	1101	1101	903	853	853	858	1258	503	803	803
	15	12	9	15	9	10	10	10	10	10	12	12	12	12	15	9	15	9	14	12	14	12	드	14	12	12	10	9	12	12
	US-10-032-162-17	US-10-323-314-16	US-09-796-202-16	US-10-032-162-2	US-09-904-380-2	US-09-934-060A-4	US-09-934-060A-2	US-09-934-060A-6	US-09-934-060A-30	US-09-934-060A-24	US-10-190-435-127	US-10-190-435-4	US-10-190-435-141	US-10-190-435-148	US-10-235-994-2	US-09-765-519-2	US-10-032-162-15	US-09-864-761-34590	US-10-003-035-55	US-10-286-332A-55	US-10-003-035-53	US-10-286-332A-53	US-09-746-783-142	US-10-003-035-33	US-10-286-332A-33	US-10-190-435-150	US-09-922-543-1	US-09-759-841-4	US-10-190-435-135	US-10-190-435-134
•	17,	Sequence 16, Appl	16,	e 2	Sequence 2, Appli	4	'n	6	30,	Sequence 24, Appl	127	Sequence 4, Appli	141	148	е 2	2, ~	e 1	34590	55,		53,		142,	33,		150,	ъ Ф	4, 1	135,	Sequence 134, App

## ALIGNMENTS

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; Sequence 2, Application US/09892949
Publication No. US2003096339A1
; GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuijper, Joseph L.
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                                                                                                                                                                                                                                   WUMBER OF SEQ ID NOS: 93
SOFTWARE: Fast SEQ for Windows Version
SEQ ID NO 2
LENGTH: 732
TYPE: PRT
ORGANIEM: Homo sapiens
US-09-892-949-2
                                                                                                                                        Query Match 100.0%; Score 1017; DB 11; Best Local Similarity 100.0%; Pred. No. 4.8e-97; Matches 189; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/267,963
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  61
                                                                                         1 KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
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Whitmore, Theodore E
Kuijper, Joseph L
Maurer, Mark F
VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI 120
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GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Presnell, Scott R.

APPLICANT: Presnell, Scott R.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Whitmore, Joseph L.

APPLICANT: Waurer, Mark P.

TITLE OF INVENTION. CYTOKINE RECEPTOR ZCYTOR17

FILE REFERENCE: 00-42

CURRENT FILING DATE: 2001-06-26

PRIOR APPLICATION NUMBER: US/09/892,949

PRIOR APPLICATION NUMBER: US 60/214,282

PRIOR APPLICATION NUMBER: US 60/214,282
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CURRENT APPLICATION NUMBER: US/09/972,708

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 745

TYPE: PRT
ORGANISM: Homo sapiens
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Best Local (
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APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: DuBose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OP INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
FILE REPERENCE: 3160-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
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Pred. No. 2.6e-96;
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APPLICANT: Mosley, Bruce A.

APPLICANT: Bird, Timothy A.

APPLICANT: Bird, Timothy A.

APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR
FILE REFERENCE: 3160-B

CURRENT APPLICATION UNDER: US/09/972,708

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 29

NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                   US-09-892-949-54
; Sequence 54, Application US/09892949
; Publication No. US20030096339A1
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                                                                                   GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presmell, Scott R.
APPLICANT: Gao, Zeren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 662
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SOFTWAKE: FASTSEQ for Windows Version
SEQ ID NO 46
LENGTH: 649
TYPE: PRT
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Best Local Similarity 94.2%;
Matches 97; Conservative
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Best Local Similarity
                                             APPLICANT:
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PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
                           APPLICANT:
      OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
                                                                                                                                                                                                                                                                                                                                                                                557 KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
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                     Gao, Zeren
Whitmore, Theodore E
Kuijper, Joseph L.
Maurer, Mark F.
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Pred. No. 8.5e-45;
1; Mismatches 2; Indels
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616

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PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 54
           RESULT 7
US-09-972-708-12
Sequence 12, Application US/09972708
Publication No. US20030059871A1
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SEQ ID NO 17
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GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
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APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
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ORGANISM: Homo sapiens
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Pred. No. 8.5e-45;
1; Mismatches
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Pred. No. 8.5e-45;
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; SEQ ID NO 12
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-972-708-12
                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-09-972-708-14
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                                                                                                                                     Query Match
Best Local Similarity 100.
Conservative
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Best Local Similarity 56.0%; Pred. No. 1.6e-41;
Matches 107; Conservative 20; Mismatches 57
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CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
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CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert P.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
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617 VIDKLYVNFGNVLQEIFTDEARTGQE
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                    61 VIDKLVVNFGNVLQEIFTDEARTGQE 86
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: Cosman, David J.
: Mosley, Bruce A.
: Bird, Timothy A.
                                                                                                   KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
                                                                            KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL
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                                                                                                                                                                       45.4%; Score 462; DB 11; 100.0%; Pred. No. 2.4e-39;
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  642
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Query Match
Best Local Similarity
Thes 62; Conserve
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; ORGANISM: Homo sapiens
US-10-006-265-2
                                                                                                               ; ORGANISM: mus musculus
US-09-892-949-57
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Best Local Similarity 100.
Matches 86; Conservative
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SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 2
                                                                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 57
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
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PRIOR TILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1099-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sprecher, Cindy A. APPLICANT: Presnell, Scott R. APPLICANT: Gao, Zeren APPLICANT: Whitmore, Theodore
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APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
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CURRENT FILING DATE: 2003-01-06
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 93
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                                                                                                                                                            LENGTH: 662
TYPE: PRT
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                       Conservative
                                                                                                                                                                                                                              for Windows Version
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                29.9%; Score 304; DB 11;
58.5%; Pred. No. 6.9e-23;
14. Mismatches 26;
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APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBURG, BSTEPILTA J.
TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV
TITLE OF INVENTION: POLYMPETIDES, POLYMPETIDES AND USES T
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF ESQ ID NOS: 319
SOFTWARE: Patentin Ver. 2.0
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US-10-190-435-128
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LENGTH: 854
TYPE: PRT
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APPLICANT: ZUR MEGEDE, Jan
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Best Local Similarity
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 GIKPVVSTQLLLNG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 CVTLNCTNATVNYNNTSKDMKNCSFYVTTELRDKKKKKENALFYRLDIVPLNNRKNGNINN 183
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                                                                                                                                                                                                                                                                   BARNETT,
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22.3%; Pred. No. 0.5;
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US-09-891-609-4
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                                   US-09-891-609-2
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                                                    RESULT 14
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SOFTWARE: PatentIn version
SEQ ID NO 4
LENGTH: 619
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09891609 Patent No. US20020127238A1
Sequence 2, Application US/09891609 Patent No. US20020127238A1
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Best Local (
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CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stamatatos, Leondias
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING
FILE REFERENCE: 2570-1-002N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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                                                                                                                                    VPDHLCEEG 160
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                                                                                                    213
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24.9%; Pred. No. 0.83;
ative 23; Mismatches
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22.3%; Pred. No. 0.
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APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCOING ANTIGI
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES ANI
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT FILING DATE: 2002-12-30
JUMBER OF SEQ ID NOS: 319
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 140
LENGTH: 865
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: TV008c4.3
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APPLICANT: ZUR MEGEDE, Jan
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING
FILE REPERENCE: 2570-1-002N
CURRENT APPLICATION NUMBER: US/09/891,609
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,608
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 4
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TYPE: PRT
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LTPLCVTLNCSDVIPSNVTNTTVT--HNNI-TDKEEMRNCTFN--
                            LVIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPE 119
                                                                 THACVETDENEQUIVLENVTENFNMWK-NDMVDQMH----EDIISLWDQSLKPCV----K 120
                                                                                               THICWPTVPNPAB-----SSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARNETT, St
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Pred. No. 0.88;
3; Mismatches 66;
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Pred. No. 2.7;
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Search c Job time	뫄	Ş
Search completed: August 18, 2003, 13:33:23 Job time : 26.0245 secs	165 ITDXXSKEYAIFYRLDVVP 183	120 IPPRKSQYLRSRMPEGTRPEAKEQLLFSGQSLVP 153

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Result
No.
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Maximum Match 10
Listing first 45
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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358
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VCLJND
S54384
VCLJSC
JC5765
AB1258
AB3503
JC6121
VCPVV2
                                                                                                                                                                                                                  AB0137
T12016
S31493
T33172
                                   VCLJKX
A35797
VCLJKB
I49699
A49511
JC1168
VCLJZR
T09448
S33850
A49377
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A44257
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                                                                      env polyprotein pr
glycoprotein 130 -
transcription fact
transcription fact
                                          env polyprotein pr
envelope glycoprot
fibronecin-binding
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interleukin-6 sign
dihydrolipoamide S
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probable DNA-bindi
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B-lymphocyte-induc
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                                                                                                                                         transcription fact
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                                                                                                                                coat protein VP1 -
                                                                                                                                                                                                                                                                 env polyprotein
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VCLJLV H72422 T04789

env polyprotein

ein pr prote prote prote

RESULT 2
A44257
interleukin-6 signal transducing molecule gp130
C;Species: Rattus norvegicus (Norway rat)

rat

involucrin -

twitchin [similari			6839	7.6	77	5
protein unc-22 (im	A88852		6831	7.6	77	4
zinc metalloprotei	E97944		1876	7.6	77	3
probable SCARECROW	T02736		1336	7.6	77	2
probable multiubiq	T51000		303	7.6	77	Ë
adaptor protein in	T09194	N	1270	7.6	77.5	0
mating-type switch	T43656		971	7.6	77.5	9
hypothetical prote	S54461		960	7.7	78	8
env polyprotein pr			856	7.7	78	37
catalase C [import	AC3220		713	7.7	78	8
85K c-Cbl-interact			665	7.7	78	5
transcription fact			358	7.7	78	34
hypothetical prote	T49648		2298	7.7	78.5	ü
related to yeast z	T39006		938	7.8	79	2
	T38616	N	771	7.8	79	μ
hypothetical prote	B86214	N	423	7.8	79	30

## ALIGNMENTS

Ş 밁 뭉 C;Superfamily: type 8 retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-520/Product: coat protein gp120 #status predicted <CP1>
F;521-856/Product: coat protein gp41 #status predicted <CP2>
F;684-705/Domain: transmembrane #status predicted <TMN>
F;87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611 A;Reference number: A44963; MUID:89228766; PMID:2713163 A;Accession: A44963 A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 28-May-1999
C;Accession: A44963
R;Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.;
A;DS Res. Hum. Retroviruses 5, 121-129, 1989
A;Title: Molecular characterization of HIV-1 isolated from a serum collected env polyprotein precursor - human immunodeficiency vin N,Alternate names: coat polyprotein N,Conteins: coat protein gp120; coat protein gp41 C;Species: human immunodeficiency virus type 1, HIV-1 Ś Ş A;Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394 C;Genetics: RESULT A44963 밁 A;Gene: env A;Molecule type: DNA A;Residues: 1-856 <SRI> Matches Query Match Best Local Similarity 135 190 130 CHNITIKDNNTNVDTEMKEEIKNCSYNMTTELRDKQRKIYSLFYRLDIVPIGGNSSNGDS 94 57 70 7 THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPC--STP-----49; ---GTRPEAKEQLLFSG 148 SKYRLINCNTSAITQACP-KVSFEPIPIH-YCAPAGFAILKCRDEEFEGKGPCRNVSTVQ NGY--VTC---PFRPDCPLGKSFEELPVSPEIPPRKSQYLRSRMPE----SDKLVIDKLVVNFGNVLQE-----IFTDBARTGQE------THACVPTDPNPQELSLGNVTEKFDMWKNNMVEQMHEDVISLWDQSLKPCVKLTPLCVTLS 129 CTHGIRPVVSTQLLLNG Conservative 9.5%; human immunodeficiency virus type 1 (isolate Z321) 20; Score 96.5; DI Pred. No. 1.6; 20; Mismatches DB 1; 71; Length 856; Indels serum collected in 1976: nu Getchell, J.; McCormick, 57; NNLGGEK 93 Gaps 247 189 56

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A; Gene: sucB
C; Superfamil
C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                       dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) [imported] - Yersinia pestis (stra C;Species: Yersinia pestis (stra C;Species: Yersinia pestis (stra C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001 C;Accession: AB0137 C;Accession: AB0137 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 1, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone
C;Superfamily: cytokine receptor homology
C;Keywords: transmembrane protein
F;134-315/Domain: cytokine receptor homology <
                                                                                                                                                                                                                                                          A;Residues: 1-407 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89957.1; PID:g15979181; GSPDB:GN00175
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-407 <KUR>
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A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number; AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0137
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Best Local
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                                                         PDLPESVADGSVATWH------KKPGDSVK-RDEVLVEIET--DKVILE-VPASQD
                                                                                          PTVP-NPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDKLVVNFG
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Pred. No. 3
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Pred. No. 1.
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A; Residues: 1-495 < CLE>
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A; Residues: 1-852 < M
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env polyprotein - human immunodeficiency virus type 1 (5Species: human immunodeficiency virus type 1, HIV-1 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #t C;Accession: S31493 R;Clegg, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H. AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein A;Reference number: 217379; MUID:98178716; PMID:9519894
A;Accession: T12016
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3) C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T12016
R;McCutchan, F.E.; Sanders_Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard,
                                                                                                                                                                                       A;Cross-references: EMBL:Z19533; NID:g60244; PIDN:CAA79593.1; PID:g60245 C;Superfamily: type E retrovirus env polyprotein C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: S31493 A; Accession: S31493 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
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                                 THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK
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THACVPTDPNPREIELENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLN 103
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                                                                                                                                                                                                                                                                                                                                                                                         Library,
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                                                                                                                  Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87.5;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                            December
                                                                                              Mismatches
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                                                                                                                                            DB 2;
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                                                                                              Gaps
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RESULT 7
H83448
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dihydrolipoamide succinyltransferase (E2 subunit) PA1586 [imported] - Pseudo C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004586; (A;Experimental source: strain PAO)
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                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-409 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: CESP:M01B12.5
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                                                                                               Query Match
Best Local Similarity
                                                                  Matches
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M.; Graves, T.; Ozersky, P.
Mor: Data Library, May 1998
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CTDNWGN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRKMVA--VWAEKEMRNLARMHEVGLPVPKPHLL-KGHVLVMDFLGKDGWPAPLLKNANL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVLQE---IFTDEA-----RTGQENNLG------GEKNGYVTCPFRPDCPLGKSF 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNPAESSIAT --- WHGDDFKDKLNLKESDDSVN-TEDRILKPCSTPSDKLVIDKLVVNFG
   PTVP-NPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDKLVVNFG
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                                                                                                                                                                                  dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70/1; 94/1; 122/3; 190/2; 260/2; 301/3; 372/2
                                                                  Conservative
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se: strain Bristol N2; clone M01B12
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                                                                                               8.5%;
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                                                                                            Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas,
                                                                  Mismatches
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                                                                                                                         DB 2;
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                                                                                                                            Length 409
                                                               Indels
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Larbig,
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K.; Lim,
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                                                                                                                                                                                                                                                                               RESULT 9
S54384
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C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-29/Domain: signal sequence #status predicted <SIO>
F;30-501/Product: coat protein gp120 #status predicted <CP1>
F;502-846/Product: coat protein gp41 #status predicted <CP2>
F;502-520/Domain: transmembrane #status predicted <TM1>
F;674-692/Domain: transmembrane #status predicted <TM2>
F;677-129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606
                                                                                                                     envelope polyprotein - human immunodeficiency virus type (;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_C;Accession: S54384
R;Theodore, T.; Buckler-White, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: coat polyprotein N;Contains: coat protein gp120; coat protein gp41 C;Species: human immunodeficiency virus type 1, H
                               submitted to the EMBL Data A; Reference number: S54377 A; Accession: S54384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-846 <S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: J00066
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi,
Gene 81, 275-284, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note:
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VLABIIKNEGDTVLSNELLGKLNEGGAAAPAAP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVLQEIFTDEARTGQENNLGGEKN-GYVTCPFRP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----MPEGTRPEAKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLV-SEKLPEH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THACVPTDPNPQEIELENVTENFNMWKNNMVEQMHEDIISLWDQSLKPC-----VKLTP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%; Score 86; DB 1; Length 846; llarity 20.2%; Pred. No. 14; Conservative 23; Mismatches 74; Indels
                                                                                            Library,
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                                                                                            July 1989
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A;Title: Envelope sequences o
A;Reference number: A28922; M
A;Accession: B28922
A;Molecule type: DNA
A;Residues: 1-861 <GUR>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A/Gene: env
C/Superfamil
C/Keywords:
F/1-29/Domai
F/30-861/Pro
F/87,129,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC: N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997 C;Accession: B28922 R;Gurgo, C:; Guo, H:G:; Franchini, G:; Aldovini, A:; Collalti, E:; Farrell, Virology 164, 531-536, 1988
RESULT
VCLJSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA
A; Residues: 1-853 < THB>
A; Cross-references: EMBL: M22639;
C; Superfamily: type E retrovirus
C; Keywords: polyprotein
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Best Local S
Matches 29
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Best Local S
Matches 49
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;Superfamily: type E retrovirus env polyprotein;
;Reywords: capsid protein; cata protein; glyprotein; polyprotein; transmembran
;1-29/Domain: signal sequence #status predicted <SIG>
;30-861/Product: env polyprotein #status predicted <EPP>
;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                   VTLNCTNLRNDTSTNATNT-TSSNRGKMEGGEMTNCSF 162
                                                                                                                                                                                                                                                                                                                                               THLCWPTVPNPAESSI -- ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHGIRPVVSTQLLLNG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNYRLINCNTSAITQACP-KVSFEPIPIH-YCAPAGFAILKCRDKRFNGTGPCTNVSTVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -IDKLVVNF----GNVLQEI-------FTDEARTGQENNLGG
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                                                                                                                                                                                                                                                                                                            THACVPTDPNPQEVVLGNVTENFNMWKNNMVEQMHEDIISLWDQSLKPCV----KLTPLC
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of two new United States HIV-1 isolates MUID:88219542; PMID:3369091
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Pred. No. 14;
28; Mismatches
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env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                   Score 86; DB 1; Length 861
Pred. No. 14;
9; Mismatches 42; Indels
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                                                                                              #text_change
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: JC5765
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1258 <PES>
A;Cross-references: GB:Y14385; NID:g2653423; PIDN:CAA74743.1;
C;Comment: This enzyme plays a role in metabolism of inositol C;Cuperfamily: SAM homology; SH2 homology
C;Keywords: phosphoric monoester hydrolase
F;21-117/Domain: Cstalytic #status predicted <CAT>
F;427-729/Domain: cstalytic #status predicted <CAT>
                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-718 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99544.1; PID:g16410895; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
C;Genetics:
A;Gene: lmo1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein lmo1466 [imported] - Listeria C;Species: Listeria monocytogenes C;pate: 27-Nov-2001 #sequence_revision 27-Nov-2001 C;Accession: AB1258 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dominguez-Bernal, G.; Duchaud, E.;
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AB1258
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                               114 LPVSPEIPPRKSQYLRSRMPEGTRPEAKEQL----LFSGQSLVPDHLCEEGAPNPYLKNS
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                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDKLVVNFGNVLQEIFTDEA-----
                                      VTAREF----LVSEKLP 182
                                                                          ALVSYAIVP--NEVYDEEQTDARRKEAAQSVVPVKILQGQVIV---
                                                                                                                                                                                                                                                                        KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKL-NLKESDDSVNTEDRILKPCSTPSDK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAKEQLLFSGQSLVPDHLCEEGAPNPY-----LKNSVTAREFLVSEKLP
ETYROLKMLHLLDOKMP
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                    ----PAPAPTST----
                                                                                                                                                                                                                                                                                                                               8.3%;
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                                                                                                                                                                                                                                                                                                               29;
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289
                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85.5;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Durand, L.; Dussurget,
                                                                                                                                                                                                                                                                                                                                   84.5; |
. No. 15;
                                                                                                                                                                                                                                    -EDKLKNIKDKLSS-NVSEKITSNISDEVFT
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                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.; Baquero, I
Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocytogenes
                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1258;
                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:e1188709; phosphate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PTG-RP
                                                                                                                                                                                                                                                                                                               45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEAGAKSKAP 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.; Berche, P.; Bloecker
Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Voss, H.; Wehland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maitournam,
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                                                                              272
                                                                                                                   169
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                                                                                                                                                                                                                                                                                                               11;
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phosphatidyl
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A;Accession: A41928
A;Status: nucleic acid seqn
A;Molecule type: mRNA
A;Residues: 198-341 <ELS>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus
C;Date: 06-Jan
C;Accession: A:
R;Turner Jr.,
Cell 77, 297-3
                                                                   A;Gene: pit-1
C;Superfamily: transcription factor Pit-1; homeobox homology; POU domain homology C;Keywords: DNA binding; homeobox; nucleus; pituitary; transcription regulation F;199-266/Domain: POU domain homology <POU>F;199-266/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: transcription factor GHF-1
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text
C;Accession: JC6121; A41928
R;Majumdar, S.; Irwin, D.M.; Elsholtz, H.P.
R;Majumdar, S.; Irwin, D.M.; Elsholtz, H.P.
Broc. Natl. Acad. Sci. U.S.A. 93, 10256-10261, 1996
A;Title: Selective constraints on the activation domain
A;Reference number: JC6121; MUID:96413633; PMID:8816787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
JC6121
                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U55045; NID:g1621540; PIDN:AAB17254.1; PID:g1621541 R;ElBinoltz, H.P.; Majumdar-Sonnylal, S.; Xiong, F.; Gong, Z.; Hew, C.L. Mol. Endocrinol. 6, 515-522, 1992 Mol. Endocrinol. 6, 515-522, 1992 A;Title: Phylogenetic specificity of prolactin gene expression to conservation A;Reference number: A41928; MUID:92261606; PMID:1350055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 77, 297-306, 1994
A;Title: Blimp-1, a novel zinc finger-containing protein A;Reference number: A53503; MUID:94221646; PMID:8168136
A;Accession: A53503
                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-358 <MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription factor Pit-1 - chinook salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: JC6121
Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
Residues: 1-856 <TUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Mus musculus (house mouse)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
                                                                                                                                                                                                                                               Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A53503
  Local Similarity
les 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 SVKEILKLDSNPSKRKDIYRSNISPFTLEKDMDGFRKNGSPDMPFYPRVVYPIRAFLPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 PIPANOELLVWYCRDFAERLHYPYPGELTVINLTQTESNPKQYSSEKNELYPKSVPKREY 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VIDKLVVNFGN---VLQEIFTDEAR--TGQENNLGGEKNGYVTCPFRP-----DCPLGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                 1-358 <MAJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.A.; Mack, D.H.; Davis, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTAREFLYSEKLPEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEELPVSPEIPPRKSQYL-RSRMPEGTRPEAKEQLLFSGQSLVPDHLCEEGAPNPYLKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNPAESSIATWHGDDFKDKL------NLKESDDS---VNTEDRILKPCSTPSDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSP----LAPGLPEH
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ilarity 22.1%;
Conservative 3
    Conservative
                 8.2%;
25.3%;
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                                                                                                                                                                                                                                                     not
    15;
Score 83.5; D
Pred. No. 7.7;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 22;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84;
Pred. No.
                                                                                                                                                                                                                                                   shown;
                                                                                                                                                                                                                                                   not
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                                       DB 1;
                                                                                                                                                                                                                                                 compared with
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  58;
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                                       Length 358;
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                                                                                                                                                                                                                                               conceptual
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  Gaps
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7;
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Search Job tir

rch completed: August time : 27.4869 secs

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2003, 13:31:22

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C; Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Parvovirus genome: A;Reference number: A03695; A;Accession: A03699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A03699
R;Rhode III, S.L.; Paradiso,
J. Virol. 45, 173-184, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coat protein VP1 - parvovirus H1
C;Species: parvovirus H1
C;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
VCPVV2
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                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X01457; EMBL:J02198 C;Superfamily: parvovirus coat protein
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-722 < RHO>
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                              Ouery Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                            Local Similarity
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 370
                                  138
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                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                           4 NKLTHICWPTVPNPAESSI----ATWHGDDFKDKLNLKESDDSVNTEDRILKPCS----
TIGEPOALNSQFFTIENTLPITLLRTG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQTRILQTCSVPHPNM---
                                                                    MVALDSNNILPYTPAAQTSETLGFYPWKPTAPAPYRYYFFMPRQLSVTSSNSAEGTQITD 369
                                                                                                                                                                       -----TPSDKLVIDKLV--VNFGNVLQEIFTDEARTGQENNLGGE-----KNGYVTC- 99
                                                                                                                                                                                                         SRLLHLGMPPSENYCRVTVHNNQTTGHGTKVKGNM-----AYDTHQQIWTPWSLVDAN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLGYTQTNVGEALAAVHGSEFSQTTICRFENLQLSFKNACTLKAIL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPLGKSFEELP---VSPEIP--PRKSQYLRSRMPEG----TRPEAKEQLLFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEDRILKPCSTPSDKLVIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPD
                                                                                                                                       AWGVWFQPSDWQFIQNSMESLNLDSLSQELFNVVVKTVTEQQGAGQDAIKVYNNDLTACM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSLSHSFPPLPPAVLSEESPLGGNKDLRLRSRPPDDPPNMDSPQIRELEKFANDFKLRRI 212
                                                                                                                                                                                                                                                                              Conservative
                                PEAKEQLLFSGQSLVPDHLCEEG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOSTABDH-----
                                                                                                                                                                                                                                                                                          20.8%;
                                                                                                    PFRPDCPLGKSFEELPVSPEIP-----PRKSQYLRSRMPEGTR--- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence of H-1 MUID:83112183; PMID:6823009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.R.
                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                          Score 83.5; DE Pred. No. 19; 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNGANTLQGSLAPCLYKFQEHGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LCEEGAPNPYLKNSVTAREFL
                                                                                                                                                                                                                                                                                                                BB
                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 08-Apr-1994
                                                                                                                                                                                                                                                                                                          Length 722;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mapping
                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of its genes by hybri
                                                                                                                                                                                                                                                                              Gaps
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Title:
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MEDLINE=93052397; PubMed=1427893;
Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
"Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule, gp130.";

Genomics 14:666-672(1992).
-i-FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
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20; Mismatches
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CDANITI-N
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SMART; SM00060;
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                                                                                                                                                                                                                                                                              DOMAIN
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SIMILARITY: Contains 1 immunoglobulin-like C2-type domain SIMILARITY: Contains 5 fibronectin type III domains SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Heterodimer of an alpha and a beta
SUBCELLULAR LOCATION: Type I membrane prote:
TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND TRANSDUCES THE SIGNAL. DOES NOT BIND EMBRYONIC DEVELOPMENT (BY SIMILARITY).
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                  709
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95
                                  61
                                                                     11
                                                                                                Similarity
                                   VIDKLVVNFGNVLQEIFTDE--ARTGQENNLGG-
                                                                     WPTVPNPAESSIATW------HGDDFKDKL--NLKESDDS-VNTEDRILKPCSTPSDKL
---GYVTCPFRPDCPLGKSF---
                 WPNVPDPSKSHIAQWSPHTPPRHNFNSKDQMYSDANFTDVSVVEIEANNKKPC--PDDLK
                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002996; CR1A.
IPR003961; FN_III.
IPR003529; Hemtopoptn_L_F2
                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
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48
134
172
457
457
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83
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157
205
226
382
                                                                                       Conservative
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22.7%;
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                                                                                      Score 93; DB
Pred. No. 2.5;
28; Mismatches
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FIBRONECTIN TYPE-III
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P17482; Q9H1I1;
01-AUG-1990 (Rel. 15, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                     MEDLINE=90215256; PubMed=2576652;
Boncinelli E., Acampora D., Pannese M.,
Gaudino G., Stornaiuolo A., Cafiero M.,
"Organization of human class I homeobox
Genome 31:745-756(1989).
                                                                                                                                                                                     "Differential expression of human HOX-2 genes along the posterior axis in embryonic central nervous system."; Differentiation 40:191-197(1989).
                                                                                                                                                                                                                                          Giampaolo A., Acampora D., Zappavigna V., D'Esposito M., Care A., Faiella A., Storna Simeone A., Bonoinelli E., Peschle C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Gr
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Submitted (NOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Kosaki K., Kosaki R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homeobox protein Hox-B9 HOXB9 OR HOX2E.
                                                                                                                                                   SEQUENCE OF 185-250 FROM N.A.
                                                                                                                                                                                                                                                                                                     MEDLINE=89378558; PubMed=2570724;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 173-250 FROM N.A.
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FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
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, Faiella A.,
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P04581;
13-AUG-1987
13-AUG-1987
16-OCT-2001
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DNA_BIND 18
CONFLICT 17
                                                                                                         13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains:
glycoprotein (GP120); Transmembrane glycoproteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Nuclear.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS A:
5-9 WEEKS FROM CONCEPTION.
-i--SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
                                           Human immunodeficiency virus
Viruses; Retroid viruses; Ret
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Pfam; PF04617; Hox9 act; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
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EMBL; AY014295; AAG42144.1;
EMBL; BC015565; AAH15565.1;
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InterPro; IPR000047; HTH_lambrepressr.
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MEDLINE-86245056; PubMed=2424612;
Alizon M., Wain-Hobson S., Montagnier L.,
"Genetic variability of the AIDS virus: n
of two isolates from African patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of two isolates from Cell 46:63-74(1986)
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EMBL; A07108; CAA00616.1;
HIV; K03454; ENV$ELI.
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InterPro; IPR000777; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PP00517; GP41; 1.
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BY 
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21; Mismatches
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HIV; M21138; ENV$JH3.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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"Nucleotide sequences of gag and env genes of HIV-1 and their expression in bacteria.",
AIDS Res. Hum. Retroviruses 5:411-419(1989).
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NCBI_TaxID=11694;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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                            MEDLINE=90034200; PubMed=2806917;
Spire B., Sire J., Zachar V., Rey F., Barre
Hampe A., Chermann J.C.;
"Nucleotide sequence of HIV1-NDK: a highly
human immunodeficiency virus.";
Gene 91:275-284(1989).
-i- MISCELLANEOUS: NDK, ISOLATED FROM A ZAI
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This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst
                                                                                      SEQUENCE FROM N.A.
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EMBL; M27323; AAA44873.1; --
PIR; JQ0066; VCLJND.
HIV; M27323; ENV$NDK.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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TRANSMEMBRANE GLYCC
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01-OCT-1989 (Rel. 12, Last sequence
16-OCT-2010 (Rel. 40, Last annotatic
Envelope polyprotein GP160 precursor
glycoprotein (GP120); Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Theodore T., Buckler-White A.;
Submitted (NOV-1988) to the HIV data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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Interpro; IPRO00777; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PP00517; GP41; 1.
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HIV; M22639; ENV$Z2Z6.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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RESULT 8
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains:
glycoprotein (GP120); Transmembrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=88219542; PubMed=3369091;

Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalt

Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;

"Envelope sequences of two new United States HIV-1 isol

Virology 164:531-536(1988).
-i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC
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HIV; M17450; ENV$SC
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Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine
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Best Local S
Matches 33
Eukaryota; Metazoa;
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CATALYTIC A
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Pfam; PFO1702; TIGRO0430; Q tRNA_tgt; 1.
TIGRFAMs; TIGRO0430; Q tRNA_tgt; 1.
Queuosine biosynthesis; Transferase; Glycosyltransferase
W tRNA processing; Zinc; Complete proteome.
T ACT_SITE 94 94 BY SIMILARITY.
T ACT_SITE 276 BY SIMILARITY.
FT METAL 313 313 ZINC (BY SIMILARITY).
FT METAL 318 318 ZINC (BY SIMILARITY).
FT METAL 318 318 ZINC (BY SIMILARITY).
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MEDLINE=2166373; PubMed=11792842;

Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashi
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi
"Complete genome sequence of Clostridium perfringens, a
flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
                      PRD1 MOUSE STANDARD; PRT; 856 AA. 606036; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) PR-domain zinc finger protein 1 (Beta-interferon regulatory domain I binding factor) (BLIMP-1). PRDM1 OR BLIMP1. Protection of the protein 1 (BLIMP-1) PRDM1 OR BLIMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003192; BAB81651.1; -.

HAMAP; MF_00168; -; 1.

InterPro; IPR004803; QtBNA_ribo_trans.

InterPro; IPR002616; tRNA_ribo_trans.

Dfan. BE01702; TGT. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
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COFACTOR: Binds 1 zinc ion
SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAS with GU(N) anticodons (tRNA-Asp, -Asn, and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, result in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 -INQGGVYEDIRIEHAKTIREMDLDGYAIGGLA-----VGETHEEMYRVIDAVVPHL
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Chordata; Craniata; Vertebrata; Euteleostomi;
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25.8%;
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QUEUINE TRNA-RIBOSYLTRANSFERASE
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InterPro; IPRO07087; Znf C2H2.

Pfam; PP000856; SET; 1.

ProDom; PD000003; Znf C2H2; 1.

SMART; SM00317; SET; 1.

SMART; SM00317; SET; 1.

SMART; SM00315; Znf C2H2; 4.

PROSITE; PS0028; ZINC FINGER C2H2 1; 4.

PROSITE; PS0028; ZINC FINGER C2H2 2; 4.

PROSITE; PS0028; ZINC FINGER C2H2 2; 4.

PROSITE; PS0028; ZINC FINGER C2H2 1; 4.

PROSITE; PS0028; ZINC FINGER C2H2 2; 4.
                                                                                                                                                                                                                                                                                                                 Metal-binding; Nuclear protein; Romain 118 237 SET.

ZN FING 606 628 C2H2-
ZN FING 634 656 C2H2-
ZN FING 662 684 C2H2-
ZN FING 662 684 C2H2-
ZN FING 660 712 C2H2
SEQUENCE 856 AA; 95835 MW; B9
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"Characterization of the B lymphocyte-induced maturation protein-1 (Blimp-1) gene, mRNA isoforms and basal promoter.";
Nucleic Acids Res. 28:4846-4855(2000).
-!- FUNCTION: Transcriptional repressor that binds specifically to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94221646; PubMed=8168136; Turner C.A., Mack D.H., Davis M.M.; Turner C.A., Mack D.H., Davis M.M.; "Blimp-1, a novel zinc finger-containing protein that can maturation of B lymphocytes into immunoglobulin-secreting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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HSSP; P08048; 7ZNF.
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NCBI_TaxID=10090;
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281
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AF305535;
AF305536;
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                                                                                                                                                                                                                                        Similarity
                                               VIDKLVVNFGN--VLOEIFTDEAR--TGQENNLGGEKNGYVTCPFRP-----DCPLGKS
                                                                                                  PIPANOELLVWYCRDPAERLHYPYPGELTVINLTQTESNPKQYSSEKNELYPKSVPKREY
SVKEILKLDSNPSKRKDIYRSNISPFTLEKDMDGFRKNGSPDMPFYPRVVYPIRAPLPED
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C2H2-TYPE.
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M; B9AC6FC2E29ECF4A CRC64;
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                                                                                                                                                                                                                                      Score 84;
Pred. No.
                                                                                                                                                                                                            Mismatches
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RESULT 11
COAT PAVHH
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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mi, PP00740; Parvo_coat; 1.

t protein; Glycoprotein. COAT
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A03699; VCPVV2.
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protein VP1 [Contains: Coat pro
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Similarity 20.8%;
43; Conservative 2:
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01-FEB-1991 (R...
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        ul-FEB-1991 (Rel. 17, Created)
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15-SEP-2003 (Rel. 42, Last annotation
Envelope polyprotein GP160 precursor [
glycoprotein (GP120); Transmembrane olenv.
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York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
"Human immunodeficiency virus type 1 cellular host range,
replication, and cytopathicity are linked to the envelope region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR000777; GP120.
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M38427; ENV$SF33
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r [Contains: Exterior membrane
glycoprotein (GP41)].
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GO; GO:0005634; C:nucleus; NAS.
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GO; GO:0006915; P:apoptosis; NAS.
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Opipari A.W. Jr., Boguski M.S., Dixit V.M.;
Opipari A.W. Jr., Boguski M.S., Dixit V.M.;
"The A20 cDNA induced by tumor necrosis factor alpha encodes a n type of zinc finger protein.";
J. Biol. Chem. 265:14705-14708(1990).
-1- FUNCTION: Interacts with NAF1 and inhibits TNF-induced NF-ka dependent gene expression by interfering with an RIP- or TRA mediated transactivation signal. Inhibitor of programmed cel death. Has a role in the function of the lymphoid system and contribute to the in vivo effects of TNF (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                  type of 2 J. Biol.
                                                                EMBL; M59465; AAA51550.1;
PIR; A35797; A35797.
Genew; HGNC:11896; TNFAIP3
MIM; 191163; -.
                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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Opipari A.W. Jr.,
"The A20 cDNA indu
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                 between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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                                                                                                                                                                                                              INDUCTION: By TNF-alpha. SIMILARITY: Contains 1 OTU domain.
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01-FEB-1991
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15-SEP-2003
InterPro; IPR000328; I
InterPro; IPR000777; C
Pfam; PF00516; GP120;
Pfam; PF00517; GP41; 1
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=90317877; PubMed=1695254;
Stevenson M., Haggerty S., Lamonica
                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Eglycoprotein (GP120); Transmembrane glycoprotein
                                                                                                                                                                 cytolysis.";
                                                                                                                                                                          variants
                                                                                                                                                                                                                                         NCBI_TaxID=11704;
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Viruses; Retroid viruses; Ret
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                                      1AIK; 16-JUN-97.
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Virology 189:534-546(1992).
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Shimizu H., Hasebe F., Tsuchie H.,
Kitamura T.;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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1017
1 KKPNKLTHLCWPTVPNPAES......VTAREFLVSEKLPEHTKGEV 189
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Copyright (c) 1993 - 2003 Compugen Ltd.
sp_plant:*
sp_rodent:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	BG	ID	Description
۲	1017	- 1	732	4.	Q8NI17	Q8ni17
N	483.5	47.5	716	11	Q8KSB1	Q8k5b1
w	479.5		235	片	Q8BSU3	Q8bsu:
4.	479.5		716	11	Q8R501	Q8r50
υı	115		801	15	Q99BY7	Q99by
6	115		801	15	Q99BX7	2995x
7	104.5		503	15	Q74827	Q74827
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9	104		501	15	Q75939	Q7593
10	103		501	15	Q75937	Q7593
11	103		501	15	Q75942	Q75942
12	102.5		791	15	Q99BX1	xd660
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14	99.5		865	15	8MQ06Q	
15	99	9.7	800	15	099871	Q90qm
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## ALIGNMENTS

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61 VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI 120 	1 KKPNKLTHLCWPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKL 60	Query Match 100.0%; Score 1017; DB 4; Length 732; Best Local Similarity 100.0%; Pred. No. 6.2e-89; Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KECEPCOT. SEQUENCE 732 AA; 82953 MW; 30F84BD3DD99A20E CRC64;	FIRM; FF00041; IN3; 1. SMART; SM00060; FN3; 3.	Pro; IPR003961;	EMBL; AF486620; AAMZ/958.1; ~. InterPro: IDR002996: CR1A.	277:16831-16	, and Activates STAT-3 and STAT-5.";	"A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals	1988187; PubMed=11877449;	SEQUENCE FROM N.A.	[1] - [4X1D=2000]	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	receptor.	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	(TrEMBLrel. 22,	01-OCT-2002 (TrEMBLrel. 22, Created)	•	OSNI17 PRELIMINARY; PRT; 732 AA.	ርሻ 1 17

Length

7;

Gaps

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166 120 106 60

224 178 annotation

of.

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SEQUENCE FROM N.A.

MEDLINE=21988187; PubMed=11877449;

MEDLINE=21988187; PubMed=11877449;

Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A.,

Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A.,

"A Novel Type I Cytokine Receptor Is Expressed
"A Novel Type I Cytokine Receptor and STAT-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8K5B1;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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EMBL; AF486621; AAW27959-1; -.

MGD; MGI:2180511; Glmr.

InterPro; IPR00396; FCRIA.

InterPro; IPR003961; FNIII.

Pfam; PF00041; fn3; 1.
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Mammalia; Eutheria;
  SEQUENCE
                                   NCBI_TaxID=10090;
                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                           Query Match
Best Local S
Matches 107
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8R501;
Q8R501;
01-JUN-2002
01-JUN-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2002) to the EMBL; AB083111; BAB88745.1; MGD; MGI:2180511; Glmr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nomura H., Yaguchi N., "Polymorphism between (receptor NR10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLMR OR NR10.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 235 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,70 full-length cDNAs";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine receptor NR10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Pituitary;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK030512; BAC26998.1; -.
                                                                                                                                                                                                                                                                                                                          SMART; SM00060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                      nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
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                                                                                                                                                                                                                                                                                                                                              PF00041;
                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107;
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                                                                                                                                                                                         Similarity 56.0
07; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                      RKPNRLTPLCCPDVPNPAESSLATWLGDGFK-KSNWKETGNSGDTEDVVLKPCPVPAD--
                                                 VIDKLVVNFGNVLQEIFTDEARTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPRKSQYLRSRMPEGTRPEAKEQLLFSGQS--LVPDHLCEEGAPNPYLKNSVTAREFLVS
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                    LIDKLVVNFENFLEVVLTEEAGKGQASILGGEANEYVTSPSRPDGPPGKSFKEPSVLTEV
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IPR003961; FN_III.
0041; fn3; 1.
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                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                            FN3;
                                                                                                                                                                                                                                                                                  80598 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25133 MW;
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56.0%;
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21,
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                                                                                                                                                                                         Score 479.5; |
Pred. No. 2.3e
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
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Last annotation updat
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Pred. No. 5.
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nd Balb/c i
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                                                                                                                                                                                                               .3e-37;
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                                                                                                                                                                                                                                 DB 11;
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on functional annot
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                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel cytokine
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Length

716; 7;

Gaps

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Q99HIT 5
Q99H Q99H
AC Q9H
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RESULT 6
Q99BX7
ID Q99B
AC Q99B
DT 01-J
DT 01-J
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Best Local S
Matches 58
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JCT-2002 (TrEMBLrel. 22, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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"Biological and immunological characteristics of HIV-1 scerebrospinal fluid and blood.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF322195; AAK09402.1; -.
                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ptam;
AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
                                                                                                                                              Q99BX7;
01-JUN-2001
                                                                                                                                                                                             Q99BX7
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Viruses;
                           Human immunodeficiency virus
                                                                     Envelope
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InterPro; IPR000777; GP120.
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  Retroid
                                                                        glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                 TK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQYLRSRMPEGTRPEAKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLVSEKLPEH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NNLGGEKNGYVTC---PFRPDCPLGKSFEELPVSPEIP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             801
801 AA;
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protein; Glycoprotein; Polyprotein; Transmembrane.
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                                                                                                                                                                                             PRELIMINARY;
viruses;
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                                                                        (Fragment)
  Retroviridae; Lentivirus.
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Pred. No. 0.
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RESULT 7
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01-NOV-1996
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Q74827;
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EMBL; AF322205; AAK09412.1; -
                                                                                                                                                      Pfam, PF00516; GP120; 1.
AIDS; Coat protein; Glyconon_TER 503 503
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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                                                                                                                                                                                                                     EMBL; U43110; AAA85201.1; -
InterPro; IPR000777; GP120.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CAR isolate
                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                 Submitted (DEC-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                          Blouin J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Envelope glycoprotein
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THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK 64
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5 (TrEMBLrel. 01,
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lycoprotein gp120
                                                                                                                                    503 AA;
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23.6%; Pred. No. 0.15;
Live 27; Mismatches
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Matches 41
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Q75939;
Q1-NOV-1996
Q1-NOV-1996
Q1-OCT-2002
                       SEQUENCE FROM N.A. STRAIN=Brazil; Ranjbar S., Holmes
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"Molecular Charaterization of HIV-1 isolate Fr
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ
EMBL; L35492; AAA72447.1; -.
                                                                                                                                                                                              Human immunodeficiency virus
Viruses; Retroid viruses; Ret
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AIDS; Coat protein; Glycoprotein.
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Viruses; Retroid viruses; Ret
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01-NOV-1996
   "Molecular Charaterization
                                                                                                                                                            NCBI_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
(Clone B1BR002W.01062aED) proviral 5' ORF (Fragment).
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                                                                                                                                                                                                                                                                                              -1996 (TrEMBLrel. 01, Created)
-1996 (TrEMBLrel. 01, Last sequence update)
-2002 (TrEMBLrel. 22, Last annotation update)
B1BR002W.01022aED) proviral 5 ORF (Fragment)
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   of HIV-1 isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104; DB 15; Length 501;
Pred. No. 0.16;
4; Mismatches 71; Indels 2
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3J databases.
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Brazil.";
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RESULT 11
Q75942
ID Q7594
AC Q7594
DT 01-NC
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Best Local Similarity
Matches 41; Conserv
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Best Local Similarity
Matches 40; Conser
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InterPro; IPRO00777; GP120.
Pfam; PF00516; GP120; 1
AIDS; Coat protein; Glycoprot
NON TER 501 501
Q75942;
Q75942;
01-NOV-1996
01-NOV-1996
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Q75937;
01-NOV-1996
01-NOV-1996
01-OCT-2002
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InterPro; IPRO00777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycopr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular Charaterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Brazil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Clone B1BR002W.01012aED)
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ER 501 501
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(TrEMBLrel. (TrEMBLrel.
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   sequence update)
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Human immunodeficiency virus 1.
Viruses, Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVIDKLVVNFGNVLQEIFTDEARTGQENNLGGE-KNGYVTCPFRPDCPLGKS-----F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKITPICVTLN--CSDVNTTNTNTSSWENMGGEIKN----CSFNITTSIGKKVRKDYALF
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                                                                                                      VPIDNAKNTTSYMLINCNTSVITQACPKISFEP---IPIHYC
                                                                                                                                           SP-EIPPRKSOYLRSRMPEGTRPEAKEOLLFSGQSLVPDHLC 157
                                                                                                                                                                                        ICVTLN--CSDVNTTNTNTSSWENMGGEIKN---
                                                                                                                                                                                                                          LVVNFGNVLQEIFTDEARTGQENNLGGE-KNGYVTCPFRPDCPLGKS-----
                                                                                                                                                                                                                                                                                                           THICWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THACVPTDPNPLEVVL----ENVTENFNMRKNNMVEQMHEDIISLWDQSLKPC-----
                                                                                                                                                                                                                                                                       THACVPTDPNPQEVVLENVTENFNMKNNMVEQMHEDIISLWDQSLKPC---
                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 103; DB 25.3%; Pred. No. 0.2; Live 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 104; DB: 24.0%; Pred. No. 0.16; Live 25; Mismatches

    Last sequence update)
    Last annotation update)
    proviral 5' ORF (Fragment).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of HIV-1 isolate F1
e EMBL/GenBank/DDBJ
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                                                                                                                                                                                        -CSFNITTSIGKKVRKDYALFNRLDV
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3J databases
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"Biological and immunological characteristics of HIV-1 subtype E cerebrospinal fluid and blood.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF322201; AAK09408.1; -.
InterPro; IPR000277; GP170.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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"Evidence for two distinct sub-subtypes within the HIV-1
                                                                                                                                                                                                                                                                    Pfam; PF00516; GP120; 1. Pfam; PF00517; GP41; 1.
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"Biological and immunological characteristics of HIV-1 s
cerebrospinal fluid and blood.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF32221; AAK09418.1; -.
InterPro; IPR000277; GP120.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glyco
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"Molecular Charaterization of HIV-1 isolate From Brazil.";
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; L35491; AAA72446.1;
InterPro; IPR000777; GP120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVNFGNVLQEIFTDEARTGQENNLGGE-KNGYVTCPFRPDCPLGKS-----FEELPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPIDNAKNTTSYMLINCNTSVITQACPKISFEP---IPIHYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THACVPTDPNPQEVVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPC-----VKITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THICWPTVPNPAESSI - - ATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDK
                                                                                                                                                                                                                                                                                                                                            protein; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 AA;
                                                                                                                                                                                                                                                                        791 AA;
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence
(TrEMBLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                   791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501
                                                                                                                                                                                                                                                                        89550 MW;
                                                                                                                                                                                                  10.1%;
21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56427 MW; B6BEC500741883A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retroviridae;
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                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 103; DB
Pred. No. 0.2;
24; Mismatches
                                                                                                                                                                                                Score 102.5; DI
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                        A2C337158E9871FB CRC64;
                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                          Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
                                    -FTDEARTGQEN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                          DB 15;
                                                                                                                                                                              73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of HIV-1 subtype
                                                                                                                                                                                                                                                                                                                                            Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                        791;
                                                                                                                                                                            81;
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RESULT 13
Q74304
ID Q7430
AC Q7430
AC Q7430
DT 01-WC
DT 01-OC
DE Envel
GN ENV-
OS Humar
OC Virus
OX NCBI
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RP SEQUI
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Best Local S
Matches 58
                                                                                               Q90QM8 PRELIMINARY; PRT; 865 AA.
Q90QM8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q74304;
Q74304;
01-NOV-1996
01-NOV-1996
01-OCT-2002
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                                                                            Envelope glycoprotein (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
     Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
NON_TER 515 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THLCWPTVPNPAESSI--ATWHGDDFKDKLNLKESDDSVNTEDRILKPC--STP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRPDCPLGKSFEELPVSPEIPPR-----KSQYLRSRMP-----EGTRPEAKEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSDYLKNDTNTTEIANCSFNINTNIRDKVQEYALFYKIDVVPIGNDNSTRYRLRSCNTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THACVPTDPNPQEIALGNVTENFNMWKNSMVEQMHEDIISLWDQSLKPCVKLTPLCVTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLNG-SLAEESVVIRSENFTNNAKTIIVQLNESVAINCIRPNNNTRKSIHIGPGRAFYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITQACP-KVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPCKNVSTVQCTHGIRPVVSTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SDKLVIDKLVVNFGNVLQEIFT-------DEARTGQENNLGGEKNGYVTCP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVOCTHGIKPVVSTQLLLNG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNG----YVTCP---FRPDCPLGKSFEELPVSPEIPPRKSQYLRS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57626 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB
Pred. No. 0.41;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5AF783BA2498A619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----HLCEEGAPNPYLKNSVTAREFLVSEKLPEHTK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15;
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OM protein - protein search, using sw model

August 18, 2003, 13:12:37; Search time 9.12114 Seconds (without alignments) 417.649 Million cell updates/sec

Title: Perfect score: US-09-892-949-2\_COPY\_520\_543 109

1 IILITSLIGGGLLILIILTVAYGL 24

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Database : A_Genes	Listing
A Geneseq 19Jun03:* 1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:* 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*	Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

v	o	7	6	ហ	4.	w	.2	بر	Result
FOT.	109	109	109	109	109	109	109	109	Score
T00.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query
662	662	662	652	652	649	627	620	581	Query Match Length DB
2	23	22	23	22	23	24	22	24	DB Bd
ABB05741	AAE24029	AAB51244	AAE24028	AAB51242	ABB05738	ABP54366	ABG05070	ABP54367	ID
Human zcytor17 pro					Human zcytor17 pro	Human NR10.5 splic		Human NR10.6 splic	Description

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AAY39993	AARROTEZ	AAR27792	AAU91240	AAB21698	AAW48734	AAR53753	AAM48227	AAG71830	ABP95678	AAG01911	AAW97363	AAW34001	AAG91861	ABP51564	AAE25071	ABU11168	ABR01682	AAU85272	AAU95704	ABJ04725	ABP95651	AAG71872	AAU24652	ABJ03986	ABB62996	AAE24037	ABP54371	ABP54370	ABB05742	ABP54365	ABP54364	AAE24024	57	ABP54363
Human CXCR4 protei	Chemokine superfam	latelet fa	Human 7 transmembr	7TM		Seven transmembran	G-protein coupled			Human secreted pro	A partial CXCR4B p	Fusin receptor ant	C glutamicum prote	Human G protein co	Human G-protein co	Human G-protein co	Human G protein co	G-coupled olfactor	Human olfactory an	GPCR 5 protein SEQ	Human GPCR polypep			Human G-protein co	7	Mouse haematopoiet			zcytori	NR10.4			zcytor1	Human NR10.3 splic

# ALIGNMENTS

RESULT 1 ABP54367

ABP54367 standard; Protein; 581 AA

ABP54367;

20-JAN-2003 (first entry)

Human NR10.6 splicing variant protein SEQ ID NO:10.

NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic cell regulation.

Homo sapiens.

WO200277230-A1.

03-OCT-2002.

22-MAR-2002; 2002WO-JP02769.

26-MAR-2001; 2001JP-0087298.

(CHUS ) CHUGAI SEIYAKU KK.

Maeda M, Yaguchi N, Hasegawa M;

WPI; 2003-018925/01. N-PSDB; ABQ83367.

NR10 splicing variants of hematopoietin receptor proteins and encoded

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RESULT 2
ABG050700
ID ABG0
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                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polynucleotides and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutal responsible for genetic disorders or other traits and to assume the contract of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostics, forensics, responsible for genetic
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23-AUG-2000; 2000US-0649167.
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                        quantitating a
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naging; diagnostic; genetic disorder.
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Matches 24
                                        The present invention describes haematopoietic receptor NR10 splicing variants (1). (1) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymocleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                  NR10 splicing variants of hematopoietin receptor proteins and encoding genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases -
                                                                                                                                                                                                    Claim 1; Fig 10-12; 250pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                          Maeda
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Query Match
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                                                                       proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple pancreatitis, and inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention.
                                                Sequence
                                                                                                                                                                                                                                                                                     The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17
                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 195-197; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotide encoding a cytokine useful for treating and diagnosing lymphoid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2000; 2000US-214282P
29-JUN-2000; 2000US-214955P
08-FEB-2001; 2001US-267963P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001; 2001WO-US20484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inrection; immunosuppression; cytotoxicity;
autoimmune disease; rheumatoid arthritis: m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscular; lymphoid; immune; inflammatory; spleenic; blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2cytor17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-090519/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 5; 5q11; cytokine receptor; mmatory; antiviral; antirheumatic; anti-
                                                                                                                                                                                                                                                                                                                                                                                     blood or
                                                649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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Score 109; DB 23; Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                  receptor zcytor17 which is , immune, inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukopenia; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarthritic;
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                649;
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AAE24028 ID AAE2

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RESULT 5
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Matches 24
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                                                                                                                                                                                                                                                                                                      The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10:1. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies and haematopoietic disorders including autoimmune diseases and allergies
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 3-5; 127pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hematopoietin receptor protein NR10 for screening potential ligands for treatment of immune and hematopoietic disorders such as autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC92337
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30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmembrane; immune disorder; haematopoietic disorder; autoimmune disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                       and pollen allergy.
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99JP-0217797.
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Pred. No. 1.3e-07;
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23-SEP-2002
variant protein
                              (first entry)
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#2.

pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; ostooporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility; ischaemic disease; variant. Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;

Homo sapiens

WO200229060-A2

11-APR-2002

05-OCT-2001; 2001WO-US31634.

06-OCT-2000; 2000US-238706P. 13-OCT-2000; 2000US-240476P. 20-FEB-2001; 2001US-270282P.

(IMMV ) IMMUNEX CORP

Mosley BA, Bird TA, Dubose RF, Wiley SR

WPI; 2002-330172/36

Human and murine hematopoietin receptor polypeptides HPR1 and HPR2, useful for treating cell proliferation, metabolic, and reproductive hormone related conditions

Disclosure; Page 110-112; 136pp; English.

The present invention relates to human and murine haematopoietin receptor collections of the invention are useful for collections cell proliferation conditions e.g., pancytopaenia, lukopaenia, canaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone cells. HPR sequences are useful for treating medical conditions and concologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancerical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancernical and cancerial and cancers, anaemia, prostate, renal cell, cell, carcinoma, carcinoma, haematologic disorders, anaemias (e.g., anaemia cell carcinoma), haematologic disorders, anaemias (e.g., anaemia cell carcinoma), haematologic disorders, anaemia, myelo-cupations, cancerial cell vasces blastic anaemia, prototiva aplastic anaemia, prototiva anaemia cell carcinoma (e.g., acatemia), colon, trombocyto-paenic purpura (ITP), sickle cell vascoclusive crisis, myelofibrosis/ cell carcinoma cell cell carcinoma cell cell cell vascoclusive crisis, myelofibrosis/ cell cell vascoclusive cri is human for treating various other disorders such as osteoporosis, deficient mammary development and infertility. The present

RESULT 8 AAE24029

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-061720/07.
N-PSDB; AAC92350.
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30-JUL-1999;
                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
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533 IILITSLIGGGLLILILTVAYGL 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Fig 13-14; 127pp; Japanese.
                        1 IILITSLIGGGLLILIILTVAYGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHUGAI RES INST MOLECULAR MEDICINE INC
                                                                                                                                                                                                                                                          metal and pollen
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99JP-0217797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                           100
                                                                                                                           .0%; Score 109; DB 22; .0%; Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                       allergy.
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Pred. No. 1.
                                                                                                   Mismatches
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.3e-07;
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CC metastasis, osteoporosis resulting from an excess of bone-resorbing colls. HPR sequences are also useful from an excess of bone-resorbing and conditions and conditions. They are useful for treating medical conditions and concologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal concologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal concologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal concologic and ovarian cancers, lung cancer (SCIC and NSCIC), including correct (SCIC and NSCIC), including carcernal, carcinoma, carcinoma, fatigue, solid tumours (e.g., osteosarcoma, carcinoma), carcinoma, fatigue, solid tumours (e.g., anaemia) myeloc squamous cell carcinoma), haeematologic disorders, anaemias (e.g., anaemia) myeloc chaptastic syndromes (including refractory anaemia, refractory anaemia concernative purpura (ITP), sickle cell vasocclusive crisis, myeloc paenic purpura (ITP), sickle cell vasocclusive crisis, myelocid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, periodontitis cresulting in tooth loosening or loss, prosthesis loosening after joint creplacement, neurodegenerative conditions (e.g., acute polyneuropathy, compassible dementia including creutzfeld-Jacob disease, demyelinating neuropathy, chronic neuronal degeneration, stroke including creatively conditions, stroke including creatively conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaemic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000; 2000US-238706P
13-OCT-2000; 2000US-240476P
20-FEB-2001; 2001US-270282P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-330172/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HPR1 variant protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human and murine haematopoietin receptor polypeptides HPR1 and HPR2. Sequences of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 112-115; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cosman DJ, Mosley BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2001; 2001WO-US31634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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    HPR1 and
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HPR2 polypeptides are
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RESULT 9
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Matches
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Best Local
                  proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, panctratitts, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5g11 chromosomal region. ABA93767 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotide encoding a cytokine receptor useful for treating and diagnosing lymphoid, immune, spleenic, blood or bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2000;
08-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
antirheumatic, antiarthritic and muscular activities. The zcytor17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 204-206; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABA93808.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscular; lymphoid; immune; inflammatory; spleenic; blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human zcytor17 protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a cytokine receptor designated zcytor17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maurer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-214282P.
; 2000US-214955P.
; 2001US-267963P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiviral; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
   to ABB05745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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   sequences used in the
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inflammatory,
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RESULT 11
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ID ABP54463
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Best Local S
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                       The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.3 protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic cell regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NR10 splicing variants of hematopoietin receptor proteins and encodegenes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2;
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                                                                                                                                         IILITSLIGGGLLILIILTVAYGL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 3; 250pp; Japanese.
                                                                                                                                                                                                                                                                                                                           681 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 AA;
                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                           Score 109;
Pred. No. 1
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Pred. No. 1.3e-07;
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                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                           DB 24;
1.3e-07;
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                                                                                                                                   The present invention describes a cytokine receptor designated zcytor17. CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, cc antirheumatic, antiarthritic and muscular activities. The zcytor17 CC proteins are useful for treating and diagnosing lymphoid, immune, cc inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated cc immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain cviral infections. They are also useful for inducting cytotoxicity and creating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autolmmune diseases (e.g. Crohn's disease), cancer, celerosis), inflammatory diseases (e.g. Crohn's disease), cancer, concreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the creating content of the present invention.
                                                                                  Query Match
Best Local 9
                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders -
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N-PSDB; ABA93767.
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29-JUN-2000; 2000US-214955P.
08-FEB-2001; 2001US-267963P.
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                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 166-168; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maurer MF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001; 2001WO-US20484.
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   520
1 IILITSLIGGGLLILIILTVAYGL 24
                                                                 24;
                                                                                  Similarity
                                                                                                                                   732 AA;
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                                                                                  100.0%;
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                                                                                  Score 109; DB 23;
Pred. No. 1.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                    553..745
/note= "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This residue changes
allelic variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allelic variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allelic variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "|
139..241
                                                     614..618
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by
Asp during allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This residue changes allelic variation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
33..241
                                                                                                                                                                                                         588..592
                                                                                                                                                                                                                                                                                                                                                              533..552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33..745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "This residue changes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Cytokine receptor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Fibronectin repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "WSXWS motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "C-terminal cytokine receptor subdomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "This residue changes to Ala during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "This residue changes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "This residue changes
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                                                                                                                                                          .601
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                                                                          "Repeat
                                                                                                                                                                                                                            "Box1 conserved motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human mature HPR1 protein"
                                                                                                                                                                          "Repeat
                                                                                                                                                                                                                                                                                                                                                                                    "Extended transmembrane domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Proline-rich linker"
                       "Repeat peptide'
                                                                                                                            "Repeat
                                                                                                                                                                                                                                                                                                                                    "Core transmembrane domain"
                                                                     peptide"
                                                                                                                          peptide"
                                                                                                                                                                            peptide'
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1 IILITSLIGGGLLILIILTVAYGL

Matches Query Match Best Local

24; Similarity

100.0%; ilarity 100.0%; Conservative

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Score 109; DB 23; Pred. No. 1.5e-07; Mismatches

23;

Length 745; Indels

0,

Gaps

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CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, CC sarcoma), carcinoma (e.g., ademocarcinoma (for example, breast cancer), CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelocomes (including refractory anaemia, refractory anaemia of chronic disease, aplastic anaemia, refractory anaemia of chronic disease, aplastic anaemia, refractory anaemia of chronic disease; myelocomes (including refractory anaemia, refractory anaemia of chronic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/ myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, periodontitis creplacement, neurodegenerative conditions (e.g., acute polyneuropathy, CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeld-Jacob disease, demyelinating neuropathy, CC dementia pravis, chronic neuronal degeneration, stroke including Cc myssthenia gravis, chronic neuronal degeneration, stroke including creating various other disorders such as osteoporosis, obesity, of the present mammary development and infertility. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human and murine hematopoietin receptor polypeptides HPR1 and HPR2, useful for treating cell proliferation, metabolic, and reproductive hormone related conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000; 2000US-238706P
13-OCT-2000; 2000US-240476P
20-FEB-2001; 2001US-270282P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
Misc-difference 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cell proliferation conditions e.g., parameter, thrombocytopaenia, neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 84-87; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides HPR1 and HPR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human and murine haematopoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2001; 2001WO-US31634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-330172/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mosley BA,
745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferation conditions e.g., pancytopaenia, leukopaenia, mbocytopaenia, neurodegenerative disorders and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  631..641
/note= "Box2 conserved motif"
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allelic variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Repeat peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Repeat peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCLC and NSCLC), including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiley
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533

IILITSLIGGGLLILILITVAYGL 556

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RESULT 14
ABP54365
ID ABP54
XX ABP54
AC ABP54
XX ABP54
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XX Humar
XX WR10;
$\mathcal{KW}$ NR10;
$\mathcal{KW}$ NR10;
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                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NR10 splicing variants of hematopoietin receptor proteins genes, applicable in searching hematopoietic factors and cremedies for immunological and hematopoietic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic cell regulation.
    NR10; splicing variant; haematopoietin receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease;
                                              Human NR10.4 splicing variant protein SEQ ID NO:6
                                                                              20-JAN-2003
                                                                                                          ABP54365
                                                                                                                                    ABP54365 standard; Protein; 764
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2001; 2001JP-0087298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2002; 2002WO-JP02769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-2003
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                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                             552
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                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                           IILITSLIGGGLLILIILTVAYGL 24
                                                                                                                                                                                                          IILITSLIGGGLLILIILTVAYGL 575
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                                                                                                                                                                                                                                                                                                                            764 AA;
                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative (
                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasegawa
                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                 Score 109; DB 24;
Pred. No. 1.5e-07;
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                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                764;
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RESULT 15
ABB05742
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Best Local S
Matches 24
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26-JUN-2000; 2000US-214282P
29-JUN-2000; 2000US-214955P
                                                                                                                                                                intection; immunosuppression; autoimmune disease; rheumatoid
                                                                                                                                                                                          antiinflammatory; antiviral; antirheumatic; antiarthritic;
muscular; lymphoid; immune; inflammatory; spleenic; blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-018925/01.
N-PSDB; ABQ83365.
                                        26-JUN-2001; 2001WO-US20484
                                                                   03-JAN-2002
                                                                                                                        Mus musculus.
                                                                                                                                                                                                                       Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
                                                                                                                                                                                                                                                  Mouse zcytor17 protein SEQ ID NO:57.
                                                                                                                                                                                                                                                                              01-MAY-2002
                                                                                                                                                                                                                                                                                                         ABB05742;
                                                                                                                                                                                                                                                                                                                                   ABB05742 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 7-9; 250pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001; 2001JP-0087298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2002; 2002WO-JP02769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haematopoietic disease; haematopoietic cell regulation
                                                                                              WO200200721-A2
                                                                                                                                                  inflammatory disease; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200277230-A1
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                                                                                                                                                                                                                                                                                                                                                                                                      552 IILITSLIGGGLLILILITVAYGL 575
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 IILITSLIGGGLLILIILTVAYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109;
Pred. No. 1.
                                                                                                                                                                cytotoxicity; leukopenia; Crohn's disease;
l arthritis; multiple sclerosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                   inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                     bowel disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764;
                                                                                                                                                                                            bone;
                                                                                                                                                                                                            cytostatic;
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08-FEB-2001; 2001US-267963P.

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Search completed: August 18, 2003, 13:27:02 Job time : 10.1211 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a cytokine receptor designated zcytor17. CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, crowder and invention and muscular activities. The zcytor17 cc antirheumatic, antiarthritic and muscular activities. The zcytor17 cc inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the crowder and the present invention.
                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders -
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N-PSDB; ABA93810.
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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PCT-US93-11153-46
US-08-202-056-3
US-08-202-056-4
US-08-701-265-4
US-08-805-478-4
US-08-805-478-4
US-08-801-238-4
US-08-801-238-4
US-08-801-228-4
US-08-118-270-346
US-09-118-270-346
PCT-US93-08528-328
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PCT-US93-08528-328
PCT-US93-08528-328
US-09-127-357-197
US-08-118-270-326
US-09-128-328-328
PCT-US93-08528-328
US-08-118-270-326
US-09-328-328-328
US-08-118-270-326
US-09-328-328-328
US-08-118-270-326
US-09-328-328-328
US-08-413-118-119
US-08-413-118-119
US-08-413-118-119
US-08-220-151-14
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US-09-299-843A-46
US-09-088-337B-46
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      Sequence
346, App
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40.4	41.3	41.3	41.3	41.3	41.3	41.3	41.3	41.3	41.3	42.2	42.2	43.1	43.1	43.1	43.1		43.1
141	370	370	370	370	370	370	370	296	258	92	92	1394	459	459	459	459	459
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US-09-328-352-6288	US-09-799-955-7	US-09-799-955-3	US-09-799-955-2	US-08-776-971-140	US-09-172-353-7	US-09-172-353-3	US-09-172-353-2	US-09-252-991A-27195	US-09-252-991A-26228	PCT-US93-08528-341	US-08-118-270-341	US-09-213-053-2	US-09-213-053-6	US-08-473-446-14	US-08-473-446-12	US-08-413-118-14	US-08-413-118-12
Sequence 6288, Ap	Sequence 7, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 140, App	Sequence 7, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 27195, A	Sequence 26228, A	Sequence 341, App	Ξ	Sequence 2, Appli	Sequence 6, Appli	Sequence 14, Appl	Sequence 12, Appl	Sequence 14, Appl	Sequence 12, Appl

# ALIGNMENTS

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; MOLECULE TYPE: protein US-08-153-848-46
Query Match
Best Local Similarity
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US-08-153-848-46
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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                               PILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5758044m1, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-0448
                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                 TELEFAX: 15-3856
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                       TYPE: ami
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                 ilarity 47.1%;
Conservative
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                                Score 49; DB
Pred. No. 24;
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Schweikart, Vicki L.

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Patent No. 63485/4
GENERAL INFORMATION:
GENERAL APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Patrick W
                                                  Sequence 46, Application US/09088337B Patent No. 6348574
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR AFFILIATION NUMBER: US 08/153,070
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/977,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 337 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gray, Patrick W. APPLICANT: Schweikart, Vicki L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jill E. Uhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godiska, Ronald
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                           45.0%;
47.1%;
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                                                                                                                                                                                                                                           Score 49; DB
Pred. No. 24;
                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                           Length 337;
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                STREET: Chicago
CITY: Chicago
TTATE: Illinois
TISA
                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Seven
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: NO. 634874and, Greta E
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 3179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
PILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
PILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
PILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 IIFLTGIVGNGLVILVM 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IILITSLIGGGLLILII 17
                                                                                                    60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312)
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                                                                                                                                                                                                                                                                                                                                                                               Application PC/TUS9311153
                                                                                                                                                                              6300 Sears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                Tower,
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                                                                                                                                                                                233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                 Transmembrane Receptors
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      Version #1.25
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US-08-202-056-3
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Best Local
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                                                                           FILING DATE: 29-MAR-1991
ATTOREX/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                              TELEPHONE: 415/252-9881
                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 25-FE
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: , 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312) 474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Noland, Greta E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genentech,
                                                                                                                                                                                                                                        25-FEB-1994
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                                                                                                              706P3
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to Human IL-8 Type B Receptor
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US-08-076-093A-4
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                                                         Matches
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      PILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-7un-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS: SOFTWARE: WinPatin (Genented CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chuntharap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 460 FULL.
CITY: South San Francisco
STATE: California
                                                                                                                                                                                        TELEFAX: 415/--7168
TELEFAX: 910/371-7168
                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 34
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                                                                                                                                                           LENGTH:
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   47
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47 IIFLTGIVGNGLVILVM 63
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                                                                       Similarity
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                                                                                                                                                                                                                      415/952-9881
                                                         Conservative
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                                                                                                                                 Linear
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                                                                                                                                                                                                                                    415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5 inch, 1.44 Mb floppy disk
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                                                                      45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Genentech)
                                                                                                                                                                                                                                                                            34,659
                                                                                                                                                                                                                                                                 706P2
                                                                       Score 49;
Pred. No.
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Pred. No.
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25;
                                                                      DB 1; Length 352; 25;
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RESULT 7 US-08-701-265-4

Sequence 4, Application US/08701265

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                                                                                                                                                                                                               Sequence 4, Application US/08284586
Patent No. 5840856
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: .
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
                                                APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Umn-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Generation Application DATA:
                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 415/225-5530
TELEPAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Love, Richard B
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE OF INVENTION:
BER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                       47 IIFLTGIVGNGLVILVM 63
                                                                                                                                                                                                                                                                                                                                                             1 IILITSLIGGGLLILII 17
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             F: 460 Point San Bruno Blvd
South San Francisco
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California
                                                                                                                                                                           Chuntharapai, Anan
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Patent No. 9
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Best Local
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                              APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chuntharapai, Anan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 11-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PU COMPACTURE SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech)
             APPLICATION NUMBER: 08/284586 FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415/2-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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South San Francisco
California
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Pred. No. 25;
6; Mismatches
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08/076093

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Best Local Similarity
Matches 8; Conserv
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APPLICANT: Lee, James
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
TELEX:
                                                                                                                           FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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LENGTH: 352 amino acid
                                                            REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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TOPOLOGY:
TELEFAX: 417, 7168
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/802,627A FILING DATE: 19-Feb-1997 CLASSIFICATION: 514
                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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South San Francisco
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                                                                                                                Love,
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                                             415/225-5530
                                                                                                              Richard B
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                                                                                          34,659
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Pred. No. 25
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TOPOLOGY:
US-08-802-627A-4
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                                                    Matches
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                                                                 Query Match
Best Local Similarity
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                                                                                                                                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/0
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-AUG-1994 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                               NAME: Love, Richard B. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 47.1 es 8; Conservative
                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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TLE OF INVENTION: PF4A RECEPTOR
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47 IIFLTGIVGNGLVILVM 63
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                         1 IIIIISLIGGGLLILII 17
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                                                                                                                                   Amino Acid
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47.1%;
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                                                                 Score 49;
Pred. No.
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Pred. No.
                                                    Mismatches
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                                                               DB
25;
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                                                                             Length 352;
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                                                    Indels
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US-08-801-228-4

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US-09-104-296-4
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                                                                         GENERAL INFORMATION:

APPLICANT: Lee, James

APPLICANT: Wood, WIlliam I.

TITLE OF INVENTION: PF4A Rece

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                                                                                                          Sequence 4, Application US/09104296
Patent No. 6087475
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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APPLICANT: Lee, James
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 4, Application US/08801228
atent No. 5922541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-D
SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION INTEREST OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 11-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 19-Feb-1997 CLASSIFICATION: 435
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COUNTRY:
                                            STREET:
                                                               DDRESSEE:
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South San Francisco
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                             South San Francisco
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Amino Acid
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USA
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SYSTEM: PC-DOS/MS-DOS
                                                          Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richard B
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                                                                                                             PF4A Receptors
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09517605
Patent No. 6391567
 Matches
                   Best
                                 Query Match
                                                                                                                   SEQ ID NO 4
LENGTH: 352
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Best Local Similarity
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                    APPLICANT: Kwon, Douglas S. APPLICANT: van Kooyk, Yvette APPLICANT: Geijtenbeck, Tneo
                                                                                                                                                                                                                                                                                                         APPLICANT: Littman, APPLICANT: Kwon, Do
                                                                                                                                                                                                                            FILE REFERENCE: 1049-1-017
                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/81
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/701265
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PRIOR APPLICATION NIMBER: 08/076093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PC com
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APPLICATION NUMBER: US/09/104,296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 352 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415/225-55:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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Similarity
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47.1%;
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                   Score 49;
Pred. No.
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Pred. No.
   Mismatches
                                   DB 4;
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                                   Length 352;
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Search completed: August 18, 2003, 13:32:22 Job time: 3.96437 secs
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US-08-118-270-346
                                                                                                                                                                    Query Match 44.0
Best Local Similarity 27.3
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSENT 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
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ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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47 || IFLTGIVGNGLVILVM 63
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419 Seventh Street, N.W., Suite 300
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Pred. No. 8.4;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                        Score
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length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07
2: /cgn2_6/ptodata/1/pubpaa/PCT1
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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gn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
gn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
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cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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US-09-972-708-14
US-10-006-265-2
US-09-972-708-15
US-09-972-708-15
US-09-892-949-54
US-10-006-265-17
US-09-972-708-4
US-09-972-708-4
US-09-892-949-57
US-09-156-761-18693
US-10-156-761-13642
US-10-156-761-13642
US-09-886-055-273
US-09-886-055-273
US-09-804-291-273
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1002.770 Million cell updates/sec
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Sequence 46, Appl Sequence 14, Appl Sequence 2, Appli Sequence 15, Appl Sequence 17, Appl Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13642, Appli Sequence 1052, Appl Sequence 1052, Appl Sequence 1052, Appl Sequence 273, App Sequence 273, App Sequence 273, App
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US-09-892-949-46

Application US/09892949

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	355	321	321	293	277	275	158	93	78	192	109	109	299	299	299	272	36	24	18	397	352	352	352	352	352	352	352	352	270	363
	15	9	9	12	9	9	10	9	9	11	15	11	12	11	10	9	11	12	15	10	15	15	12	10	10	10	10	10	12	10
	US-10-237-563-30	US-09-815-242-10635	US-09-815-242-4990	US-10-017-161-818	US-09-755-456-7	US-09-755-456-9	US-09-747-155-218	US-09-811-284-250	US-09-864-761-37650	US-09-776-724A-110	US-10-091-572-318	US-09-764-891-4763	US-10-017-161-232	US-09-804-291-41	US-09-886-055-41	US-09-755-456-10	US-09-983-802-197	-10-251-703-	US-10-084-813-127	US-09-712-363-280		US-10-225-567A-76	US-10-251-703-38	US-09-870-759-144	US-09-870-759-37	US-09-104-063-4	US-09-953-717-2	US-09-953-692-2	US-10-017-161-856	US-09-738-626-5615
	Sequence 30, Appl	10635,	990,	Sequence 818, App	Sequence 7, Appli	Sequence 9, Appli	Sequence 218, App	Sequence 250, App	37650,	Sequence 110, App	318,	4763,	232,	4	e 41,	10, Aj	197,	39, 1	127,	280	Sequence 1, Appli	76	38,	144,	37	4	2	2	856, F	Sequence 5615, Ap

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Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 93
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 46
LENGTH: 649
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                         Query Match
Best Local Similarity
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
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APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/267,963 PRIOR FILING DATE: 2001-08-02
                                                                                24;
                      1 IILITSLIGGGLLILIILTVAYGL 24
IILITSLIGGGLLILIILTVAYGL 543
                                                                                    Conservative
                                                                                  100.0%; Score 109; DB 11
100.0%; Pred. No. 9.5e-07
Live 0; Mismatches 0
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                                                                                                                             Length 649;
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US-09-972-708-15
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; ORGANISM: Homo sapiens
US-09-972-708-14
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CURRENT APPLICATION NUMBER: US/10/006,265

CURRENT FILING DATE: 2003-01-06

PRIOR APPLICATION NUMBER: PCT/JP00/03556

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: JP 11/155797

PRIOR FILING DATE: 1999-06-02

PRIOR APPLICATION NUMBER: JP 11/217797

PRIOR FILING DATE: 1999-07-30
                                  Sequence 15, Application US/09972708 Publication No. US20030059871A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 24; Conserv
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SEQ ID NO 2
LENGTH: 652
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Best Local Similarity
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SEQ ID NO 14
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APPLICANT: Cosman, David J.
APPLICANT: Cosman, David J.
APPLICANT: Wosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: DuBose, Robert F.
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APPLICANT: Yaguchi, No. US20030125520Aliko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Cosman, David J.
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100.0%; Pred. No. 9.5e-07;
tive 0; Mismatches 0;
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Sequence 17, Application US/10006265
Publication No. US20030125520A1
GEMERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006,265
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SEQ ID NO 54
LENGTH: 662
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
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Best Local (
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
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PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
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CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
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APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND
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Bird, Timothy A.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-17
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                                                                                                                     Sequence 4, Application US/09972708
Publication No. US20030059871A1
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Best Local :
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LENGTH: 732
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Publication No
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Best Local Similarity
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PRIOR FILING DATE: 2000-06-01
PRIOR DATE: 2000-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILLING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
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CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
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APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
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PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/267,963
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Similarity 100.0%; Pred. No. 1.1e-06;
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Theodore E.
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100.0%; Pred. No. 9.7e-07;
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US-09-972-708-12
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SOFTWARE: FASCESEQ for W
SEQ ID NO 57
LENGTH: 662
TYPE: PRT
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CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
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CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                       Sequence 12, Application US/09972708 Publication No. US20030059871A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 3160-B
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                                                                                                                                    APPLICANT:
                                                                                                                                                     APPLICANT: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 00-42
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CURRENT APPLICATION NUMBER: US/09/972,708
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TYPE: PRT
ORGANISM: Homo sapiens
                                    TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Maurer, Mark F.
ITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                              534 IVLLTSLVGGGLLLLSIKTVTFGL 557
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                                                   Cosman, David J.
Mosley, Bruce A.
Bird, Timothy A.
DuBose, Robert F.
Wiley, Steven R.
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ilarity 100.0%;
Conservative (
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66.7%;
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Pred. No. 0.0029;
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Pred. No. 1.1e-06;
); Mismatches 0;
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RESULT 12
US-10-156-761-13642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptomyces avermitilis US-10-156-761-8893
                                                                                                                                                                                           Sequence 13642, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IXEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8893
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 726
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                         CURRENT APPLICATION NUMBER: US/10/156,76:
CURRENT FILING DATE: 2002-05-29
                                                                                                           APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SHAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                 FILE REFERENCE: 249-262
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hes 15; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                   235 ILLTALIGGGIFVLVAYT 252
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55.6%;
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Pred. No. 5
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Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASURAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UF 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
NUMBER OF SEQ ID NOS: 2430
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Best Local Similarity
"hes 9; Conserv?
                                                        ; ORGANISM: Homo sapiens US-09-886-055-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens 
US-10-017-161-1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Streptomyces avermitilis
US-10-156-761-13642
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                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: STRYER, LUBERT

APPLICANT: ZOZULYA, SERGEY

APPLICANT: ZOZULYA, SERGEY

TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND

TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS

FILE REFERENCE: 078003-0277150

CURRENT APPLICATION NUMBER: US/09/886,055

CURRENT FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: 60/213,812

PRIOR FILING DATE: 2000-06-22
                                                                                         NUMBER OF SEQ ID NOS: 522
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 273
LENGTH: 318
TYPE: PRT
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NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13642
LENGTH: 175
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SEQ ID NO 1052
LENGTH: 302
                   Query Match
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Publication No. US20030143668A1
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Best Local (
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46.8%;
57.9%;
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42.9%; Pred. No.
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Pred. No.
 Score
Pred.
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 DB 10;
24;
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13;
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Best Local Similarity

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; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PATENTIN VET. 2.1
; SEQ ID NO 273
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ZOZGIA, SERGEY
APPLICANT: ZOZGIA, SERGEY
FILE REFERENCE: P 0278005
CURRENT APPLICATION NUMBER: US/09/804,291
CURRENT PILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,914
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 60/199,335
PRIOR APPLICATION NUMBER: 60/27,702
PRIOR APPLICATION NUMBER: 60/27,702
PRIOR APPLICATION NUMBER: 60/27,702
PRIOR APPLICATION NUMBER: 60/20,702
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/23,34
PRIOR APPLICATION NUMBER: 60/213,849
PRIOR APPLICATION NUMBER: 60/26,534
PRIOR APPLICATION NUMBER: 60/23,732
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-804-291-273; Sequence 273, Application US/09804291; Sequence 273, US20030088059A1
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Search completed: August 18, 2003, 13:33:24
Job time: 4.46873 secs
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Best Local Similarity 57.9
Matches 11; Conservative
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                                                                                                                                                                                                   46.8%; Score 51; DB 11; Length 318; 57.9%; Pred. No. 24; ative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                                                                                                                                                    seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                         283308 seqs, 96168682 residues
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1: pir1:*
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pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	φ	œ	7	თ	υ	4	ω	N	μ	No.	Result
48	48	48	48	48	48.5	49	49	49	49	49	49	49	49	49	49	49	49	50	50.5	50.5	51	51	51	51	51	51	52	55	Score	
44.0	٠	44.0	44.0	44.0	44.5	45.0	45.0		45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	45.9	46.3	46.3	46.8	46.8	46.8	46.8	46.8	46.8	47.7	50.5	Match I	Query
432	405	401	397	339	266	1124	929	539	455	413	397	368	360	353	353	352	352	366	1433	580	530	465	329	280	206	97	527	662	Length :	
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T21880	H83798	F87196	T44477	D83201	AB2270	B84742	T32492	T27559	A75121	T23766	H70789	A96929	E95273	H75265	S28787	A45747	G00048	C64449	GNVUBW	S76846	E82189	E87591	H64220	C70784	T34961	C75415	H72536	A54078	ID	
	ABC transporter (p	probable membrane-	hypothetical prote		hypothetical prote	m	-	-	•	hypothetical prote	probable serine pr	histidine kinase-l		conserved hypothet	neuropeptide Y/pep	neuropeptide Y/pep	fusin (LESTRA) - c	cationic amino aci		hypothetical prote	methyl-accepting c	sensor histidine k	membrane protein m	diheme	probable membrane	hypothetical prote	e oligopep	methyl-accepting c	Description	

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46	40	46	46	46	46	46.5	47	47	47	47	47	47	47.5	47.5	48
42.2	42.2	42.2	42.2	42.2	42.2	42.7	43.1	43.1	43.1	43.1	43.1	43.1	43.6	43.6	44.0
242	216	202	202	153	96	446	662	473	430	423	343	322	448	398	505
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A69026	H83757	JC6205	JC4635	T17893	E69790	A38244	D54078	AF1207	F70016	T26306	AD1502	A64023	F82280	B71193	B88206
ਲ	hypothetical prote	cell surface antig	tumor-associated L	hypothetical prote	hypothetical prote	citrate transport	methyl-accepting c	ABC transporters (	purine permease ho	hypothetical prote	hypothetical prote	hypothetical prote	citrate/sodium sym	hypothetical prote	protein F21D12.3 [

# ALIGNMENTS

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A;Cross-references: GB:L29189; NID:g459687
A;Cross-references: GB:L29189; NID:g459687
A;Note: the sequence in GenBank entry BACMCPTLP, release 106.0, (PID:g459688) has 360-N
A;Note: the sequence in GenBank entry BACMCPTLP, release 106.0, (PID:g459688) has 360-N
A;Note: the sequence in GenBank entry BACMCPTLP, release 106.0, (PID:g459688) has 360-N
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A;Note: the sequence in GenBank entry BACMCPTLP, release 106.0, (PID:g459688) has 360-N
A;Note: the sequence in GenBank entry BACMCPTLP, release 106.0, (PID:g459688) has 360-N
A;Note: the sequence in GenBank entry BACMCPTLP, release 106.0, (PID:g459688) has 360-N
A;Authors: Dauber, S.; Bruschi, A.; Hibert, A.; Hill, A.; Fund, S.; Hollon, S.; Hullo, M.F.
A;Authors: Lauber, D.; Fritz, C.; Pujita, M.; Fujita, Y.; Fuma, S.; Hullo, M.F.
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: Ao5580; MUID:98044033; PMID:9384377
A;Accession: H69655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Hanlon, u.m.,
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methyl-accepting chemotaxis protein mcpB - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000 C;Accession: A54078; H69655
                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-359,'N',361-449,'G',451-662 <KUN>
A;Cross-references: GB:Z99119; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15115.1; PI
A;Experimental source: strain 168
                                                                                                                                                                C; Superfamily: probable methyl-accepting chemotaxis transducer C; Keywords: chemotaxis; signal transduction; transmembrane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Cloning and characterization of genes encoding A; Reference number: A54078; MUID:94245722; PMID:8188684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                  Comment: Strains in which this protein is inactivated are defective in chemotaxis
    10;
                                                  Similarity
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                                             50.5%; Score 55; DE 55.6%; Pred. No. 11;
5
         Mismatches
                                                                                      DB 2;
                                                                                      Length 662;
         Indels
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    Gaps
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RESULT 4
T34961
               C;Accession: T34961
R;Saunders, D.C.; Harris, D.; Jame
submitted to the EMBL Data Library
A;Reference number: Z21563
A;Accession: T34961
A;Status: preliminary; translated
                                                                                                                                                    probable membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: C75415
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Date: 03-Dec-1919 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-527 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Ae A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72536
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A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-97 <WHI>
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 10
                                                                                                                              Species: Streptomyces coelicolor;Date: 05-Nov-1999 #text_change 05-Nov-1999;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: strain
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;Experimental source: strain R1
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;Accession: H72536
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Pred. No. 22;
7; Mismatches
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Pred. No. 6.6;
5; Mismatches
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                       from
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                                                                                              K.D.;
                     GB/EMBL/DDBJ
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                                                                                              Parkhill,
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T.; Zalewski,
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A;Gene: qcrC
C;Superfamily: Streptomyces coelicolor probable diheme cytochrome
C;Superfamily: Streptomyces coelicolor probable diheme cytochrome
C;Reywords: chromoprotein; heme; iron; metalloprotein
F;63-136/Domain: cytochrome c6 homology #status atypical <CYCl>
F;164-235/Domain: cytochrome c6 homology *CVCl>
F;164-235/Domain: cytochrome c6 homology *CVCl>
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                                                                                                                           C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium A;Title: The minimal gene complement of Mycoplasma genitalium A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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A; Gene: SCOEDB: SC4A10.24c
                                                                                                                                                                                                                                                                                                                                          membrane protein msmF homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-280 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                    A;Molecule type: DNA
A;Residues: 1-329 <TIGR>
                                                                                                                                                                                                                                                                                              C;Accession: H64220
R;Fraser, C.M.; Gocayne, J.D.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain C; Genetics:
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C; Accession: C70784
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C;Species: Mycobacterium tuberculosis
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A;Cross-references: EME
A;Experimental source: strain G-37
                        A;Cross-references: GB:U39696; GB:L43967; NID:g1045869; PID:g1045873; TIGR:MG188
                                                                                                     A;Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                M.; Fuhrmann, J.; Nguyen, D.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;178/Binding site: heme iron (His) (axial ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Z70283; GB:AL123456; NID:g3261561; PIDN:CAA94263.1; PID:g1237047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;73,76/Binding site: heme (Cys) (covalent) #status predicted;77/Binding site: heme iron (His) (axial ligand) #status predicted;174,177/Binding site: heme (Cys) (covalent) #status predicted
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9; Conservative
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ce: strain A3(2)
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                                                                                                                                                                                                                                                                  O.; Adams, M.D.; Clayton, R.A.; Fleischmann, ck, T.R.; Saudek, D.M.; Phillips, C.A.; Merri
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13;
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A; Experimental C; Genetics:
A; Gene: VC1535
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C;Apecies: Caulobacter crescentus
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.H.; Kolon
D; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A; Complete Genome Sequence of Caulobacter crescentus
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82189
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: E82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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C;Superfan
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A;Residues: 1-530 <HEI>
A;Cross-references: GB:AE004231;
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A; Residues: 1-465 < S'
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blai, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes
                                                                                                          cationic amino acid transporter MCAT-2 homolog - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Decies: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: C64449
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C;Genetics:
A;Map position: segment M
C;Superfamily: bunyavirus M polyprotein
C;Superfamily: bunyavirus M polyprotein
C;Keywords: glycoprotein; nonstructural protein; polyprotein;
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1433/Product: M polyprotein #status predicted <MPP>
F;60,248,624,1169/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 148, 1-14, 1986
A;Title: Nucleotide sequence
A;Reference number: A04101; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M polyprotein precursor - bunyamwera virus N;Contains: glycoprotein G1; glycoprotein G2; nonst C;Species: bunyamwera virus C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequenc
C;Accession: 876846
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A;Molecule type: genomic RNA
A;Residues: 1-1433 <LEE>
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BNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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R; Lees, J.F.; Pring
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A; Residues: 1-580 < KAN>
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C.M.; Smith, H.O.; Woese,

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neuropeptide Y/peptide YY receptor Y3 - human N;Alternate names: fusin; HM99; leukocyte-derived seven-transmembrane receptor LESTR; C;Species: Homo sapiens (man) C;Date: 03-May-1994 #sequence revision 03-May-1994 #text change 05-Nov-1999 C;Accession: A45747; A53103; E33006; I59444; I69203; S32761 R;Federsppiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Legenomics 16, 707-712, 1993 A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pa;Reference number: A45747; MUID:93315164; PMID:8325644
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A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64449
A;Status: preliminary. ......
A;Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A. DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization A;Reference number: I53006; MUID:93319629; PMID:8329116
A;Accession: I53006
                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-352 < FED>
A; Residues: 1-352 < FED>
A; Cross - references: GB: M99293; NID: g292516; PIDN: AAA16617.1; PID: A; Cross - references: GB: M99293; NID: g292516; PIDN: AAA16617.1; PID: A; Choese CB: M99293; NID: g292516; PIDN: AAAA16617.1; PID: A; Biol. Chem. 269, 232-237, 1994
A; Title: Cloning of a human seven-transmembrane domain receptor, A; Reference number: A53103; MUID: 94103215; PMID: 8276799
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A;Map position: REV1140149-1139049
C;Superfamily: probable cationic amino acid transporter MCAT-2
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A; Residues: 1-352 < LOE >
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A;Title: Sequence and expression of a neuropeptide Y receptor cDNA. Reference number: S28787; MUID:92100053; PMID:1661837 A;Accession: S28787 A;Molecule type: mRNA A;Residues: 1-353 cRIMs A;Residues: 1-353 cRIMs A;Cross-references: EMBL:M86739 C;Superfamily: vertebrate rhodopsin C;Keywords: appetite; G protein-coupled receptor; transmembrane pro
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane
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A;Molecule
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A;Residues: 1-352 <RES>
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A; Residues: 1-352 < RE2>
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R;Jazin, E.E.; Yoo, H.; Blomgyist, A.G.; Yee, F.; Weng, G.; Walker, M.W.
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#text\_change 17-Mar-2000

J.D.; Dodson, T.; Zalewski,

C. . .

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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75265
A;Accession: H75265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <WHI>
A;Residues: 1-353 <WHI>
A;Residues: 1-353 <WHI>
A;Cross-references: GB:AE002080; GB:AE000513; NID:g6460327; PIDN:AAF12054.1; PID:g646033
A;Cross-references: GB:AE002080; GB:AE000513; NID:g6460327; PIDN:AAF12054.1; PID:g646033
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CCR4 SHEEP
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PUCK BACSU
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Y410 RESA
USBB GORGO
Y705 METJA
CD2 HORSE
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INCLUDES ASPARAGINE, ASPARTATE, GLUTAMINE, AND HISTIDINE.

-I- FUNCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT, TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND PACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL OF METHYLATION. ALL AMINO ACIDS SERVE AS ATTRACTANTS IN B. SUBTILIS, THEY APPEAR TO CAUSE AN INCREASE IN THE TURNOVER METHYL GROUPS, LEADING TO METHYLATION OF AN UNIDENTIFIED ACCEPTOR, WHILE REPELLENTS HAVE BEEN SHOWN TO CAUSE A DECREASE IN METHYL GROUP TURNOVER. THE METHYL GROUPS ARE ADDED BY A METHYLESTERASE.

-I- SIMILARITY: Contains 1 methyl-accepting transducer domain.

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RESULT
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Pfam; PF002743; Cache; 1.
Pfam; PF00672; HAMP; 1.
Pfam; PF00672; HAMP; 1.
Pfam; PF00203; TarH; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00304; HAMP; 1.
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EMBL; Z99120; CAB15115.1; --
PIR; A54078; A54078.
HSSP; P02942; 10U7.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Murphy L., Gentles R., Murphy L., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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InterPro; IPR003088; Cyt CI.
InterPro; IPR000345; CytC he
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EMBL; AE007071; AAK46536.1;
PIR; C70784; C70784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
SIBUNIT: THE MAIN SUBUNITS OF THE UBIQUINOL:CYTOCHROME
ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A CYTOCHROME
-!- SIMILARITY: SOME, TO CYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey B.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Salzberg
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinon
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                                                                Conservative
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                                                                               46.8%;
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HEME 1 (COVALENT) (POTENTIAL).

HENE 1 (COVALENT) (POTENTIAL).

IRON (HEME 1 AXIAL LIGAND) (POTENTIAL).

HEME 2 (COVALENT) (POTENTIAL).

HEME 2 (COVALENT) (POTENTIAL).

HEME 2 (COVALENT) (POTENTIAL).

HEME 2 (COVALENT) (POTENTIAL).
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RESULT 3
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01-OCT-1996
28-FEB-2003
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13-AUG-1987
16-OCT-2001
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Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Mguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

"In the minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

"In the MINIMAL AND TOMESTON A BINDING-PROTEIN-DEPENDENT TRANSPORT

SYSTEM. PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT

SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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Bacteria; Firmicutes;
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TIGR; MG188; -
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TE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEMETICAL PROTECTION TRANSFER FALSE_NEMETICAL PROTECTION TO THE PROTECTIO
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                  (Rel. 05, Created)
(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
in precursor (Contains: Glycoprotein
M; Glycoprotein Gl].
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(Rel. 34, Last sequence update)
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SIGNAL
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CHAIN
CHAIN
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                                                                                                                                 15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
(Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derived seven transmembrane domain receptor) (LESTR) (Fragment).
                                                                                                                                                                                                                                                SHEEP
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InterPro; IPR005168; Bunya_G2.
Pfam; PF03557; Bunya_G1; 1.
Pfam; PF03563; Bunya_G2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VITOLOGY 148:1-14(1986).
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
-INCLUDING NONSTRUCTURAL PROTEIN NS-M, GLYCOPROTEIN G1, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=86098655; PubMed=3753629;
Lees J.F., Pringle C.R., Elliott R.M.;
"Nucleotide sequence of the Bunyamwera virus M RNA segment:
conservation of structural features in the Bunyavirus glycoprotein
                                                                 Mammalia; Eutheria;
Bovidae; Caprinae;
                                                                                            Eukaryota; Metazoa; Chordata;
                                                                                                         Ovis aries (Sheep)
                                                                                                                       EXCR4 OR LESTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- SIMILARITY: BELONGS TO THE BUNYAVIRUSES M POLYPROTEIN FAMILY.
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NCBI_TaxID=11573;
TISSUE=Hypothalamus;
Dyer C.J., Matteri R
                          SEQUENCE FROM N.A.
                                                 NCBI_TaxID=9940;
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 Keisler D.H.;
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GLYCOPROTEIN G2.
NONSTRUCTURAL PROTEIN
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SEQUENCE FROM TISSUE-Spleen;
STRAIN=Wistar; TISSUE-Spleen;
Harrison J.K., Salafranca M.N.;
"Molecular cloning of rat CXCR4.";
"Molecular cloning of rat CXCR4.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ d.
                                                                                                                                                                                                                                                                                                                                                                                                                                          CCR4_RAT
008565;
                                                                                                                                                                                                                                                                           008565;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-d
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PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                             NCBI_TaxID=10116;
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les 8; Conserv
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PTM: SULFATED (BY SIMILARITY).

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CAUTION: Was originally (Ref.1) thought to be a receptor for neuropeptide Y type 3 (NPY3-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE C-X-C CHEMOKINE SDF-1. THE C-X-C CHEMOKINE SDF-1. THE SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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5 (POTENTIAL).
BY SIMILARITY.
SULFATION (POTENTIAL).
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3 (POTENTIAL).
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2 (POTENTIAL).
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E SDF-1. TR
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                TRANSDUCES
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DCC-2001 (Rel. 40, Last annotation update)
C-X-C chemokine receptor type 4 (CXC-R4) (CXC)
(Stromal cell-derived factor 1 receptor) (Fus
                                                                                                                                                                                                                                                                                                                                         DISULFID MOD_RES
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TRANSMEM
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Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCREHODDPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane;

DOMAIN 1 36
         Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                         CERTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a large-
                                                   CXCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                           CCR4_CERTO
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SUBCELLULAR LOCATION: Integral membrane protein.
TIASUE SPECIFICITY: EXPRESSED IN NEURONS AND IN ASTROCYTES.
PIM: SULPATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO FAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. INVOLVED IN B-CELL LYMPHOPOLESIS, BOME-MARKOW MYELOPOLESIS CARDIAC VENTRICULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENIIN VASCULARIZATION OF THE GASTROINTESTINAL TRACT, PROBABLY REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES
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                                                                                                                                                                                                                                                             8; Conserv
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SULFATION
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Pred. No.
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; 7E0789A605C60C09 CRC64;
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3 (POTENTIAL)
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                                                                                                                                           352
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25;
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Cercopithecinae; Cercocebus

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CCR4 HUMAN
ID CCR4 H
AC P30951
DT 01-UUL
DT 15-SEP
DE C-X-C
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DE seven
DE (HM89)
GN CXCR4.
OS Pan tr
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Best Local S
Matches 8
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Pfam; PRO0001; 7tm 1; 1.

Pfam; PRO00217; GPCRHODDESN.

PRINTS; PR00237; GPCTEIN RECEP_F1 1; 1.

PROSITE; PS00237; G_PROTEIN RECEP_F1 2; 1.

PROSITE; PS50262; G_PROTEIN RECEP_F1 1; 1.
                                       MOD RES
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98321155; PubMed=9656999;
Chen Z., Gettie A., Ho D.D., Marx P.A.;
Chen Z., Gettie A., Ho D.D., Marx P.A.;
"Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary SIVsm, HIV-2, and SIVmac.";
Virology 246:113-124(1998).
-i- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
         Homo sapiens
                  CXCR4.
                                  seven transmembrane domain receptor)
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9531;
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troglodytes
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         (Human), and
                          antigen).
(Chimpanzee)
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                                                                                                                                                                                       Score 49;
Pred. No.
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EXTRACELLULAR (POTENTIAL)

7 (POTENTIAL)
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N-TINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                  receptor)
or) (LESTR)
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(See http://www.isb-sib.ch/announce/
L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is produced through a collaboration
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                                   (LCR1) (FB22) (NPYRL)
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                                           (Leukocyte-derived
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SPECIES=Human; TISSUE=Fetal spleen;
MEDLINS=9315164; PubMed=8325644;
Pedersppiel B., Melhado I.G., Duncan A.M., Delaney A.D.,
Schappert K.T., Clark-Lewis I., Jirik F.R.;
"Molecular cloning of the cDNA and chromosomal localization of the
gene for a putative seven-transmembrane segment (7-TMS) receptor
isolated from human spleen.";
Genomics 16:707-712(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herzog H., Hort Y.J., Shine J., Selbie L.A.; "Molecular cloning, characterization, and loc homolog to the reported bovine NPY Y3 recepto and activation.";
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96217947; PubMed=8629022;
Feng Y., Broder C.C., Kennedy P.E., Berger E.A.
"HIV-1 entry cofactor: functional cDNA cloning
transmembrane, G protein-coupled receptor.";
Science 272:872-877(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jazin B.B., Yoo H., Blomqvist A.G., Yee F., Weng G., Walker I Salon J., Larhammar D., Wahlestedt C.R.;
"A proposed bowine neuropeptide Y (NPY) receptor cDNA clone, human homologue, confers neither NPY binding sites nor NPY
                     MEDLINE=98258970;
Caruz A., Samsom N
                                                                                                                                                                                                                               Wegner S.A., Ehrenberg Michael N.L.;
                                                                                                                                                                                                                                                                        SPECIES=Human; TISSUE=Peripheral blood MEDLINE=98136183; PubMed=9468539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nomura H., Nielsen B.W., Matsushima K.;
"Molecular cloning of CDNAs encoding a LD7
leukocyte chemotactic peptide receptors.";
Int. Immunol. 5:1239-1249(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606, 9598;
[1]--
  Virelizier J.L.,
                                                                       SPECIES=Human;
                                                                                                                                                                                "Genomic organization and functional characterization of the chemokine receptor CXCR4, a major entry co-receptor for human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE=94103215; PubMed=8276799;
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                                                                                                                                       Biol.
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Pept. 47:247-258(1993).
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                                                                                                                                     273:4754-4760(1998)
M., Alonso J.M., Alcami J., Baleus Parmentier M., Arenzana-Seisdedos
                                             PubMed=9599023;
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MEDLINE=96351078; PubMed=8752281;
Oberlin B., Amara A., Bachelerie F., Bessia C., Virelizier J.-L.,
Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
Legler D.F., Loetscher M., Baggiolini M., Moser B.;
"The CKC chemokine SDF-1 is the ligand for LESTR/fusin and preventinfection by T-cell-line-adapted HIV-1.";
Nature 382:833-835(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99189752; PubMed=10089882; Parzan M., Mirzabekov T., Kolchinsky P., V Gerard N.P., Gerard C., Sodroski J., Choe "Tyrosine sulfation of the amino terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=P.troglodytes;
MEDLINE=98090115; PubMed=9430250;
MEDLINE=98090115; PubMed=9430250;
Pretet J.-L., Zerbib A.C., Girard M., Guillet J.-G., E
"Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          man: absence of a splice variant corresponding to mouse CXCR4-B human tissues.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99384048; PubMed=1045
Gupta S.K., Pillarisetti K.;
"CXCR4-Lo: molecular cloning
 Lapham
                   CHARACTERIZATION (
MEDLINE=97002453;
                                                                      Oberlin E., Amara A., Bacl
Arenzana-Seisdedos F., Scl
Legler D.F., Loetscher M.
Nature 384:288-288(1996).
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[9]
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382:829-833(1996).
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163:2368-2372(1999).
Ouyang
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18; PubMed=10452968;
                                    OF ITS
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                   PubMed=8849450,
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Nguyen N.Y.,
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Science
                                       Tatsumi M., Takahashi H.;
Submitted (JUL-1996) to the
-!- FUNCTION: RECEPTOR FOR
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2-Chemokine receptor type 4 (CXC-R4) (CXC
CSTromal cell-derived factor 1 receptor) (Fus
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                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                 Macaca fascicularis
                                                                                                                                                                                                                                                    CXCR4.
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                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=9541;
                                                                                                                                                                 Cercopithecinae;
                                                                                                                                                                                         Mammalia;
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INVOLVED IN HAEMATOPOIESIS AND IN CARDIAC VENTRICULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENTIAL ROLE IN VASCULARIZATION OF THE CASTROINTESTINAL TRACT, PROBABLY BY REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN ENDOTHELIAL CELLS. COULD BE INVOLVED IN CEREBELIAR DEVELOPMENT. IN THE CNS, COULD MEDIATE INTEPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL-NEURON SURVIVAL ACTS AS A PRIMARY RECEPTOR FOR SOME HIPPOCAMPAL SURVIVAL ACTOR SOME SURVIVA
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Name=2; Synonyms=CXCR4-LO;

IsoId=P30991-2; Sequence=VSP_001890;

Note=Has been shown to exist_only in human so far;

Note=Has been shown to exist_only in human so far;

TISSUB SPECIFICITY: Expressed in numerous tissues, such as peripheral blood leukocytes, spleen, thymus, spinal cord, heart, placenta, lung, liver, skeletal muscle, kidney, pancreas, cerebellum, cerebral cortex and medulla (in microglia as well as in astrocytes), brain microyascular, coronary artery and umbilical cord endothelial cells. Isoform 1 is predominant in all tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane ALTERNATIVE PRODUCTS:
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SIMILARITY:
                     SIGNAL
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                     ΥВ
                                                                                                                                                                                                           Metazoa;
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                     INCREASING
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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i H.;
to the EMBL/GenBank/DDBJ databases.
TO FOR THE C-X-C CHEMOKINE SDF-1. TF
SING THE INTRACELLULAR CALCIUM IONS
                                                                                                                                                                                       Primates;
                                                                                                                                                                                                           (Crab eating macaque) (Cynomolgus monkey).
Chordata; Craniata; Vertebrata; Euteleostomi;
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47.1%;
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Haggarty B., Choe
S.S., Doms R.W.,
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s., Vance P.C.
Landau N.R.,
                                           TRANSDUCES
                        LEVEL
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RESULT 10
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Best Local :
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P79394; 002745; (
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15-JUL-1998 (Rel
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SEQUENCE
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TRANSMEM
                                       SEQUENCE FROM N.A.
STRAIN=Indian macaque;
MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
         "Genetically divergent strains of CCR5 as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).
                                                                                                                    Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled DOMAIN 1
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                               Cercopithecinae;
NCBI_TaxID=9544;
                                                                                                                                                            CXCR4.
                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4)
(Stromal cell-derived factor 1 receptor) (Fusin)
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PYM: SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                             Macaca.
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simian immunodef
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Pretet J.-L., Guillet J.-G., Butor C.;
"New widespread CXCR4 allele in rhesus macaques does not predict
subspecies or clinical evolution.";
AIDS Res. Hum. Retroviruses 14:639-641(1998).

-- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINS EDF-1. TRANSDUCES
SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

--- SUBCELLULAR LOCATION: Integral membrane protein.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane;
DOMAIN 1 39 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                 DOMAIN
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EMBL; U93311; AAB54116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
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MEDLINE=97268687; PubMed=9108095;
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47.1%;
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BY SIMILARITY.

K -> B (IN REF. 2).

D -> V (IN REF. 2 AND ...

S -> N (IN REF. 2).
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                                                           Score 49;
Pred. No.
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(IN REF. 2 AND 3).
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RESULT 11 CCR4\_PAPAN

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01-MAY-1992
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P56491;
15-JUL-1998
15-JUL-1998
16-OCT-2001
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-I- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDP-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- PTM: SULFATED (BY SIMILARITY).
                                                                                                                                                                TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-UUI-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-x-C chemokine receptor type 4 (CXC-R4) (CXCR-4)
(Stromal cell-derived factor 1 receptor) (Fusin).
                                                                                                                                                                                                                                                                               G-protein
DOMAIN
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PROSITE; PS00237; GEOTEIN RECEP F1 1; 1.
PROSITE; PS50262; GEOTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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  sequence update)
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Pred. No.
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InterPro; Irac.

Pfam; PRO0001; 7tm 1; 1.

PRINTS; PRO0237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M86739; -; NOT_ANNOTATED_CDS
EMBL; AF399642; AAK94452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salon J., Larhammar D., Wahlestedt C.R.;
"A proposed bovine neuropeptide Y (NPY) receptor human homologue, confers neither NPY binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor) (Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derive seven transmembrane domain receptor) (LESTR) (LCR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                responsiveness on transfected cells.", Regul. Pept. 47:247-258(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92100053; PubMed=1661837;
Rimland J., Xin W., Sweetnam P., Saijoh K., Nestler E.J., Duman R.S.;
"Sequence and expression of a neuropeptide Y receptor cDNA.";
Mol. Pharmacol. 40:869-875(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jazin E.E., Yoo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94052833; PubMed=8234909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHOWS THAT IT IS NOT A NPY3-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IO SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER. PTM: SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. CAUTION: Was originally (Ref.1) thought to be a receptor for neuropeptide Y type 3 (NPY3-R).
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RESULT 13
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SEQUENCE FROM N.A.
MEDLINE=97404646; PubMed=9261358;
MEDLINE=97404646; PubMed=9261358;
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4)
(Stromal cell-derived factor 1 receptor) (Fusin)
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Felis silvestris catus (Cat).

Felis silvestris catus (Cat).

Felis silvestris catus (Cat).
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InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm ; 1.
PRINTS; PR00201; GPCRRHODDPSN.
PROSITE; PS00237; GPCOTEIN RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kovacs E.M., Baxter G.D., Robinson W. "Feline peripheral blood mononuclear CXC and CC type chemokines."; Arch. Virol. 144:273-285(1999).
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Submitted (DEC-1996)
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15-JUL-1998 (Re
                                                                                                                                                                       EMBL; U63558; AAC48852.1; -. EMBL; U92795; AAB51765.1; -.
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                                                                                                                                                                                                                                                                    entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Shared usage of the chemokine receptor CXCR4 by the feline immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TR SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS SUBCELLULAR LOCATION: Integral membrane protein. FIM: SULFATED (BY SIMILARITY).
                                                                                                                                                 AJ009816; CAA08839.1;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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TRANSMEM
                                                                                            Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C., Yoshid O., Matsushima K., Yoshida N., Springer T.A., Kishimoto "Molecular cloning and characterization of a murine pre-B-cell growth-stimulating factor/stromal cell-derived factor 1 recept murine homolog of the human immunodeficiency virus 1 entry cor
                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM CXCR4
TISSUE=Pre-B cell;
MEDLINE=97121456; PubMed=8962122;
                                                                                                                                                                                                           "Cloning of the mouse fusin gene,
                                                                                                                                                                                                                            STRAIN=C57BL/6J, and 129/Sv; TISSUE=Peritoneal MEDLINE=97113334; PubMed=8955194; Heesen M., Berman M.A., Benson J.D., Gerard C.
                    Schubel A.,
Submitted (
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                    chemokine receptor) (PB-CKR)
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SEQUENCE FROM N.A.
                                        STRAIN=129/Sv;
                                                   SEQUENCE FROM N.A.
                                                               Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
[3]
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                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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8; Conser
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                    9/Sv; TISSUE=Thymus;
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(SEP-1996) to the E
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(ISOFORMS CXCR4-A AND CXCR4-B)
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                    R., Lipp M.;
the EMBL/GenBank/DDBJ databases.
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Pred. No.
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N-LINKED (GLCNAC. . .
BY SIMILARITY.
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-> E (IN REF. 3).
EA2BD46068A6C05B CRC64;
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Moepps B., Frodl R., Rodewald H.-R., Baggiolini M., Gierschik P., "Two murine homologues of the human chemokine receptor CXCR4 mediating stromal cell-derived factor lalpha activation of Gi2 are differentially expressed in vivo."; Eur. J. Immunol. 27:2102-2112(1997).
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"Embryonic expression and function of the chemokine SDF-1 and its "receptor; CXCR4.";

Dev. Biol. 213:442-456(1999).

-I- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

INVOLVED IN B-CELL LYMPHOPOIESIS, BONE-MARROW MYELOPOIESIS AND IN CARDIAC VENTRICULAR SEPTUM FORWATION. PLAYS ALSO AN ESSENTIAL ROLE IN VASCULARIZATION OF THE GASTROINTESTINAL TRACT, PROBABLY BY REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zou Y.-R., Kottmann A.H., Kuroda M., Taniuchi I., Littman D.R., "Function of the chemokine receptor CXCR4 in haematopoiesis and cerebellar development."; Nature 393:595-599(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The chemokine receptor CXCR4 is essential for vascularization of the gastrointestinal tract."; Nature 393:591-594(1998).
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STRAIN=C57BL/6; TISSUE=Thymus;
Suzuki G., Nakata Y., Uzawa A.
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Heesen M., Berman M.A., Hoepken U.E., Gerard N.P.,
"Alternate splicing of mouse fusin/CXC chemokine re
cell-derived factor-lalpha is a ligand for both CX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL
STRAIN=ICR;
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J. Immunol. 158:3561-3564(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99410349; PubMed=10479460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE
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ISOId=P70658-2; Séquence=VSP 001891;
TISSUE SPECIFICITY: LYMPHOCYTES, WACROPHAGES, NEUTROPHILS,
MICROGLIAL CELLS AND ASTROCYTES. FOUND IN SPLEEN, THYMUS, BOI
MARROW, LYMPH NODES AND, AT LOWER LEVELS IN BRAIN, SMALL
INTESTINE, STOMACH AND KIDNEY. CXCR4-A IS PREDOMINANT IN ALL
                                                                                                                                                                  Name=CXCR4-A; Synonyms=LESTR-A;
                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2; Name=CXCR4-B; Synonyms=LESTR-B; IsoId=P70658-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                               ENDOTHELIAL CELLS. INVOLVED IN CEREBELLAR NEURONAL LAYER FORMATION, PREVENTING PREMATURE MIGRATION OF PROLIFERATING GRANULE CELLS FROM THE EXTERNAL ERANULE LAYER INWARDS. IN THE CNS, COULD MEDIATE HIPPOCAMPAL-NEURON SURVIVAL.
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rota S., Iizasa H., )
mura Y., Matsushima F
gasawa T.;
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K., Yoshida N., Nishikawa
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e receptor-4: stromal
CXC chemokine
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DEVELOPMENTAL STAGE: HIGH EXPRESSION DURING EMBRYONIC DEVELOPMENT DEVELOPMENT DEVELOPMENT COES NOT SEEM TO BE ASSOCIATED WITH THE DIFFERENTIATION OF ANY PARTICULAR CELL TYPE, BUT IS WIDELY UTILIZED WHEN THERE IS A REQUIREMENT FOR CELL MOVEMENT. FREQUENTLY ASSOCIATED WITH LESS IPPERRNTIATED CELL TYPES AND DOWN REGULATED WITH SUBSEQUENT DIFFERENTIATION. DETECTED IN SITES WITH HARMOPOIETIC POTENTIAL: THE YOLK SAC (7.5, 8.5 AND 12.5 DPC). BUTHER (12.5 DPC). DURING GASTRULATION, AT 7.2 TO 7.8 DPC, EXPRESSION IN THE MESODERM AND THE DEFINITIVE ENDODERM. AS GASTRULATION PATTERN PADES (8.5 DPC), EXPRESSION IN THE MESODERM IS DOWN-REGULATED, WHILE IT RECOMES PREDOMINANT IN NEURAL ECTODERM ENDODERMAL EXPRESSION IS RETAINED IN THE FOREGUT AND LATER IN A SUBSET OF FOREGUT DERIVATIVES, INCLUDING THE STOMACH (10.5 DPC), THE CYSTIC DUCTS OF THE GALLELADDER AND THE LUNG EPITHELIUM (12.5 DPC). IN NEURAL TISSUE: AT 10.5 AND 12.5 DPC, EXPRESSION MORE TIGHTLY CONFINED TO THE MENDAL EPITHELIUM LINING THE VENTRAL ROOT GANGLIA, IN THE VENTRAL EPITHELIUM LINING THE VENTRAL ROADS (RESTLUM). EXPRESSION THE DOVENDING THE DIFFCRED TO THE REGION WHERE THALAMUS AND HYPOTHALAMUS MEET.

DETECTED IN A DISCRETE BAND OF CELLS AT THE EMPOCRETING OF THE DIFFCRED TO THE REGION WHERE THALAMUS AND HYPOTHALAMUS MEET.

DETECTED IN A DISCRETE BAND OF CELLS AT THE ENDOTHELIUM OF NUMEROUS BLOOD VESSELS, BUT NOT ALL, AT 10.5, 11.5 AND 12.5 DPC, SICH BANDAUS AND HYPOTHALAMUS MEET.

DETECTED IN A DISCRETE BAND OF CELLS AT THE ENDOTHELIUM OF THE MENDAL FARMALY AND HYPOTHALAMUS MEET.

DETECTED IN A DISCRETE BAND OF CELLS AT THE ENDOTHELIUM OF THE MENDAL FARMALY SUFFICIENT OF THE CAPACITORY BULL AT 10.5, 11.5 AND 12.5 DPC, SICH BANDAUS AND HYPOTHALAMUS MEET.

DETECTED IN A DISCRETE BAND OF CELLS AT THE ENDOTHELIUM OF THE CAPACITAL WALL CAPILLARIES, FACIAL VESSELS, AND, AT 14.5 PDC, IN THE VASCULATURE OF THE OUTFLOW THE ARROWANDERS.

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culties requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                          use purposan Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entities removed.
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EMBL; U59760; AAB07725.1; -.
EMBL; U65580; AAC52953.1; -.
EMBL; D87747; BAA13451.1; -.
EMBL; Z80111; CAB02201.1; -.
EMBL; Z80112; CAB02202.1; -.
EMBL; X99581; CAA67893.1; -.
EMBL; X99581; CAA67894.1; -.
EMBL; X99582; CAA67894.1; -.
EMBL; AB000803; BAA19187.1; -.
EMBL; AB000803; BAA19187.1; -.
GO; GO:0007420; p:brain development; IMP.
GO; GO:000334; P:regulation of cell migration; IMI of the Proposition of the color of
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
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PRINTS; PR00237; GPCRRHODOPSN.
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RESULT 15
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Best Local Similarity
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           EMBL; U32805; AAC22907.1; -
PIR; A64023, A64023.
TIGR; H11248; -
Hypothetical protein; Trans
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TRANSMEM 54 74
TRANSMEM 100 120
TRANSMEM 137 157
TRANSMEM 137 157
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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen M.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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01-NOV-1995
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                                                                                                                                              modified and this statement
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                                                                                                                                                                                                                                             Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
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Pasteurellaceae; Haemophilus.
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                                                                                                                                                                      the European Bioinformatics Institute.

    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    -!- SIMILARITY: SOME, TO E.COLI YOHM AND M.JANNASCHII MJ1092.

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322 AA;
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Q8K5B1
Q8K501
Q8VGY3
Q8YBL7
Q9YBL7
Q9XZF9
Q9VJX9
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                                                                           Q8ni17 homo sapien
Q8bsu3 mus musculu
Q8k5b1 mus musculu
Q8r501 mus musculu
Q8r903 mus musculu
Q8vgy3 mus musculu
Q9vjb17 aeropyrum p
Q9xzf9 drosophila
Q9vjx drosophila
Q9nbk8 drosophila
Q9ruv1 deincoccus
Q9z5v8 streptomyce
Q925v8 streptomyce
Q98100 fusobacteri
Q8kgc3 chlorobium
Q8kgc3 chlorobium
Q8kgk2 homo sapien
Q9a4r5 caulobacter
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49.5	49.5	50	50.5	51
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Q9mzn0 alouatta se	Q9mzm8 callithrix	Q9mzp0 macaca авва	Q9mzm5 pithecia pi		Q9mzq0 pygathrix n		Q9mzp8 colobus pol		Q9mzp2 mandrillus	Q9mzm4 nycticebus	Q9mzm3 nycticebus					Q9n130 saimiri bol		Q9hl24 thermoplasm	$\mathbf{r}$	m	Q8ewi7 mycoplasma	Q92ms2 rhizobium m	7	Q8np90 corynebacte	Q8cv70 oceanobacil		P74642 synechocyst	Q9kru9 vibrio chol

## ALIGNMENTS

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RESULT 2
Q8BSU3
ID Q8BSU3
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QBN117
ID QBN11
AC QBN11
AC QBN1
AC GP13
DE G
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

( MEDLINE=21988187; PubMed=11877449;
A Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De T. Novel Type I Cytokine Receptor Is Expressed on Mor Proliferation, and Activates STAT-3 and STAT-5.";
AL J. Biol. Chem. 277:16831-16836 (2002).

DR EMBL; AF486620; AAM27958.1; -.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR003961; FN_III.

DR Pfam; PF00041; fn3; 1.

TYNNER. SM00060; FN3; 3.
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Matches 24
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OSNI17; O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                  520
                                                                                                                                                                               Similarity
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       PRELIMINARY;
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Pred. No. 5.3e-06;
); Mismatches 0;
       PRT;
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Monocytes, Signals
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RESULT 4
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01-OCT-2002 (TrEMBLre
01-OCT-2002 (TrEMBLre
01-MAR-2003 (TrEMBLre
GD130-like monocyte r
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01-MAR-2003
01-MAR-2003
01-MAR-2003
Q8R501;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21988187; PubMed=11877449;
Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A
"A Novel Type I Cytokine Receptor Is Expressed a
Proliferation, and Activates STAT-3 and STAT-5.
J. Biol. Chem. 277:16831-16836(2002).
EMBL; AF486621; AAN27959.1; -.
MGD; MGI:2180511; Glmr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN III.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 235 AA; 25133 MW;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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16; Conserv
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3 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                       716 AA;
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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66.7%;
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Pred. No. 0.0043;
5; Mismatches
                                                                                                                                                                                                                                        Score 83; DB 11; Length 716; Pred. No. 0.011;
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Sciurognathi; Muridae;
                        PRT;
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Expressed on
nd STAT-5.";
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1 Monocytes,
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Murinae; Mus
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Signals
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QBVGY3;
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Q1-MAR-2002 (TEMBLrel. 20, C)
Q1-MAR-2003 (TEMBLrel. 23, L)
Q1-MAR-2003 (TEMBLrel. 23, L)
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Submitted (Ar.
Submitted; Ab.
EMBL; AB083111; BAbu.
EMGD; MGI:2180511; Glmr.
InterPro; IPR002996; CR1A.
TOPPRO; IPR003961; FN III.
TOPPRO; IPR03391; 1.
TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPRO; TOPPR
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01-JUN-2002 (TrEMBL
01-OCT-2002 (TrEMBL
Cytokine receptor N
                                                                                                                                                                                  Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang
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                                                                                                                                                                      Receptor.
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                                                                                          Local Similarity
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                                                                         Conservative
                                                                                                                                                  AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                  35532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.1%;
                                                                                          47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maeda M., F
C57BL/6 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                         <u>ب</u>
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Pred. No.
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                                                                                          Score 52;
Pred. No.
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53
                                   19
                                                                                                                                                                                                                                                                                                                                                                                                   superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                    6308508DD931B80E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBFB718DCCD40FC7
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                                                                           Mismatches
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d Balb/c in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                     of the mouse.";
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                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae;
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                                                                                                              Length 314;
                                                                                                                                                      CRC64;
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINB=99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an acrobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE |
STRAIN=K1
                                                                                                                               EMBL; AF140019; AAD30131.1; -. HSSP; O60603; 1FYW. FlyBase; FBgn0026760; Tehao.
                                                                                                                                                                                                                              Luo C., Zh
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crenarchaeon, Aeropyrum pernix Kl."; DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 527AA long hypothetical
                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEHAO OR CG7121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XZF9;
01-NOV-1999
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                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                        Submitted
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InterPro; IPR000566; Lipocln cytFABP.
Pfam; PF00528; BPD transp; 1.
PROSITE; PS00213; LIPOCALIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aeropyrum pernix.
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=56636;
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                   interPro;
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                                                                                                                                                                                                                                                                                                                                          _TaxID=7227;
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                                                                                                                                                               Zheng L.;
und related proteins from insects.";
ed (APR-1999) to the EMBL/GenBank/DDBU databases.
            o; IPR004075; ILL_receptor1.
0; IPR001611; LRR.
0; IPR000372; LRR_Nterm.
0; IPR003591; LRR_typ.
1; IPR000157; TIR_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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12, Last sequence update)
23, Last annotation update)
oligopeptide transport syst
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12,
23,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nalson C.R., Mikloog C.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Baytkaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Harris M.X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Werherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Werherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Menten B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarma D.A., Weinstook G.M., Weinsenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
RA Zheng Y.-, Zhong F.N., Zhong W., Zhu S., Zhu X., S
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Best Local
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Q9VJX9;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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PRINTS; PR00019; LEURICHRET.
SMART; SM00013; LERRUT; 1.
SMART; SM000369; LER TYP; 2.
SMART; SM000255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEHAO protein.
TEHAO OR CG7121.
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23,
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Last annotation update)
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RESULT
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Best Local S
Matches 8
Query Match
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Pfam; PF01582; TIR; 1.
PRINTS; PR01537; INTRLEXPIRIF.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00013; LRRTY; 1.
SWART; SM00013; LRR TYP; 2.
SWART; SM00355; LRR TYP; 2.
SWART; SM00355; TIR; 1.
                                                                                             InterPro; IPR003591; LRR_typ.
InterPro; IPR00157; TIR_domain
Pfam; PF00560; LRR; 5.
Pfam; PF01462; LRRNT; 1.
Pfam; PF01582; TIR; 1.
Pfam; PF01582; TIR; 1.
PRINTS; PR01537; INTRLEXPIRIF.
PRINTS; PR010019; LEURICHRPT.
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InterPro; IPR000372; I
InterPro; IPR003591; I
InterPro; IPR000157; T
                                                                                                                                                                                                                                 expression in Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
EMBL; AF247767; AAF86227.1; -.
HSSP; O60603; 1FYW.
                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                       PROSITE; PS50506; LRR TYPICAL; 1.
PROSITE; PS50104; TIR; 1.
SEQUENCE 795 AA; 90255 MW; 3A
                                                         SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 2.
SMART; SM00255; TIR; 1.
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01-OCT-2000
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PROSITE; PS50104; TIR; 1.
SEQUENCE 795 AA; 90241 MW; 61B8839E2036E28C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0026760; Tehao.
InterPro; IPR004075; IL1_receptor1.
InterPro; IPR001611; LRR.
                                                                                                                                                                                 FlyBase; FBgn0026750; Tehao.
InterPro; IPR004075; IL11 receptor1.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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HSSP; O60603; 1FYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of Science 287:2185-2195
                                                                                                                                                                                                                                                                                   Tauszig S., Jouanguy E., Hoffmann J., In Troll-related receptors and the control
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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8; Conserv
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                        LRR_typ.
TIR_domain.
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47.78;
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Last annotation update)
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Pred. No.
Score 52;
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                        3A0883EE4A86E247 CRC64;
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B
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                                                                                                                                                                                                                                                                                   antimicrobial peptide
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Length 795;
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RESULT 11
Q9Z5V8
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Q9RUV1
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Best Local Similarity
Matches 10; Conserv
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Q9Z5V8
Q9Z5V8;
01-MAY-1999
01-MAY-1999
01-JUN-2001
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Q9RUV1;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                       STRAIN-A3(2);
Cadwallader A.B., McCormick J.R.;
Cadwallader A.B., McCormick J.R.;
I'dentification and Characterization of the Ce
Streptomyces coelicolor A3(2).";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
EMBL; AF123319; AAD20009.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Dodson R.J., Haft D.H., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.I. Makarova K.S., Aravind L., Daly M.J., Smith H.O., Venter J.C.,
Hypothetical NON_TER
                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
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TIGR; DR1280; -.
Hypothetical protein; Comple
SEQUENCE 97 AA; 10260 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein DR1280.
                                           InterPro; IPR002965; P_rich_exprints; PR01217; PRICHEXTENSN
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 16.4 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591
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(TrEMBLrel. 10,
L (TrEMBLrel. 17,
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                        protein.
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41.7%;
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Pred. No.
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D; Mismatches 4
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Zalewski C.,
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RESULT 12
Q9S2W5
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Matches 9
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Redenbach M., Kieser H.M., Lunn.
Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Line 1 Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                 Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajbandram M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                        Complete proteome. SEQUENCE 206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saunders D.C., Harris
Submitted (AUG-1999) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative membrane protein. SCO2091 OR SC4A10.24C.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                         "Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3 (2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3 (2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  InterPro; IPR002965; P_rich_ex
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21996410; PubMed=12000953;
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                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A.;
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                                                                                                                                                                                                                                                              AL939111; CAB52000.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                        IILITSLIGGGLLILIILTVA
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VLLVVVLLGGGLIGLLVLNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Parkhill J., (AUG-1999) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                                                                                                                                                                                        20899 MW;
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Pred. No.
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                                                                                                                                                                                        90131DF9AAB059D7 CRC64;
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                                                                                             Mismatches
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                                                                                                                                        Length 206;
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Best Local S
Matches 8
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01-OCT-2002
01-OCT-2002
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STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
Mapatral V., Anderson I., Ivanova N.,
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J. Bacteriol. 184:2005-2018(2002).
EMBL; AE010486; AAL93937.1; -.
                                                                                                                   Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., Debby R., Gwinm M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F., Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey I Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune I Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.; "The complete genome sequence of Chlorobium tepidum TLS, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhattacharyya A., Bartman A., Gardner W., Vasieva O., Chu L., Kogan Y., Chaga O., G Vasieva N., D'Souza M., Walunas T., Pusch Fonstein M., Kyrpides N., Overbeek R., Tonstein M., Kyrpides N., Tonstein M., Tonstein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycerol uptake
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01-JUN-2002
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                                                         photosynthetic, anaerobic, green-sulfur bacterium.", Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=TLS / ATCC 49652 / DSM 12025;
MEDLINE=22103685; PubMed=12093901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlorobium tepidum.
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Pfam; PF00230; MIP; 1.
ProDom; PD002395; MIP family; 1.
TIGRPAMS; TIGR00861; MIP; 1.
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                            AE012784; AAM71293.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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Fusobacterales; Fusobacteriaceae;
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Pred. No.
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W., Grechkin G., Zhu L
., Goltsman E., Bernal
sch G., Haselkorn R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
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Zhu
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Q8NGKZ
ID Q8NGK
AC Q8NGK
AC Q8NGK
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DE Seven
OS HOMO
OC Eukar
OC Mamma
OX NCEI
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RP SEQUE
RA Suwa
RA Tsuts
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                                                                                                                                                                                                                                                                                                                     Query Match 46.8
Best Local Similarity 57.9
Matches 11; Conservative
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QBNGK2;
QBNGK2;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
Q1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Seven transmembrane helix receptor.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor genes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB065792; BAC06011.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS0262; G PROTEIN_RECEP_F1_2; 1.
Receptor; Transmembrane.
SEQUENCE 314 AA; 35622 MW; 001831FCAA557474 CRC64;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 288 AA; 32122 MW; 4A5E26101B84C9F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,

Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;

"Genome-wide discovery and analysis of human seven transmembrane helix
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129 VLFMLAYAGGGLLIFLLLGVYYRL 152
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                                                                                                                                                                 ISYVIALLGNSLLIFILT 53
                                                                                                                                                                                                                                                                                                                                                      46.8%;
57.9%;
                                                                                                                                                                                                                                                                                                                 ; Score 51; DB 4; Length 314; ; Pred. No. 71; 3; Mismatches 5; Indels
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